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OM protein - protein search, using sw model

Run on: January 31, 2002, 11:15:59 ; Search time 23.86 Seconds

(without alignments)
139.702 Million cell updates/sec

Title: US-09-579-420-1

Perfect score: 264
Sequence: 1 PCGPCSEBRKHLFVQDPQC.....NTDSRCKAROLELNEPTCRC 45

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 522463 seqs, 74073290 residues

Total number of hits satisfying chosen parameters: 330423

Minimum DB seq length: 0
Maximum DB seq length: 100

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

A.Geneseq_1101.*
1: /SID8/gcgdata/geneseq/geneseq/AA1980.DAT.*
2: /SID8/gcgdata/geneseq/geneseq/AA1981.DAT.*
3: /SID8/gcgdata/geneseq/geneseq/AA1982.DAT.*
4: /SID8/gcgdata/geneseq/geneseq/AA1983.DAT.*
5: /SID8/gcgdata/geneseq/geneseq/AA1984.DAT.*
6: /SID8/gcgdata/geneseq/geneseq/AA1985.DAT.*
7: /SID8/gcgdata/geneseq/geneseq/AA1986.DAT.*
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16: /SID8/gcgdata/geneseq/geneseq/AA1995.DAT.*
17: /SID8/gcgdata/geneseq/geneseq/AA1996.DAT.*
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21: /SID8/gcgdata/geneseq/geneseq/AA2000.DAT.*
22: /SID8/gcgdata/geneseq/geneseq/AA2001.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	264	100.0	45	20	VEGF antagonist pe
2	255	96.6	44	14	AAV22023
3	255	96.6	44	20	AAV22023
4	250	94.7	44	17	AAV22023
5	178	67.4	41	21	AAV22023
6	138	52.3	24	20	AAV22023
7	115	43.6	21	20	AAV22023
8	115	43.6	21	20	AAV22023
9	115	43.6	21	20	AAV22023
10	76	28.8	20	14	AAV22023
11	58	22.0	62	21	AAV22023

12	58	22.0	62	21	AAV22023
13	58	22.0	67	21	AAV22023
14	58	22.0	67	21	AAV22023
15	58	22.0	67	21	AAV22023
16	58	22.0	83	21	AAV22023
17	58	22.0	83	21	AAV22023
18	58	22.0	83	21	AAV22023
19	56.5	21.4	84	22	AAV22023
20	56.5	21.4	89	21	AAV22023
21	55	20.8	53	20	AAV22023
22	54	20.5	53	20	AAV22023
23	52.5	19.9	69	22	AAV22023
24	52	19.7	68	12	AAV22023
25	52	19.7	68	13	AAV22023
26	52	19.7	68	15	AAV22023
27	51.5	19.5	53	22	AAV22023
28	51.5	19.5	53	22	AAV22023
29	51.5	19.5	53	22	AAV22023
30	51	19.3	76	22	AAV22023
31	50	18.9	67	22	AAV22023
32	50	18.9	49	21	AAV22023
33	50	18.9	49	21	AAV22023
34	50	18.9	63	21	AAV22023
35	50	18.9	69	21	AAV22023
36	49.5	18.8	100	22	AAV22023
37	49	18.6	63	20	AAV22023
38	48	18.2	35	22	AAV22023
39	48	18.2	49	21	AAV22023
40	48	18.2	49	21	AAV22023
41	48	18.2	53	19	AAV22023
42	48	18.2	53	20	AAV22023
43	47.5	18.0	57	21	AAV22023
44	47.5	18.0	26	15	AAV22023
45	47.5	18.0	58	22	AAV22023

ALIGNMENTS

RESULT 1	
ID	AAV22023 standard; peptide; 45 AA.
AC	AAV22023;
XX	
DT	26-AUG-1999 (first entry)
XX	
DE	VEGF antagonist peptide.
XX	
KW	VEGF; vascular endothelial growth factor; antagonist; neovascularisation;
KW	angiogenesis; retinal neovascularisation; haemangioma; Kaposi's sarcoma;
KW	solid tumour growth; leukaemia; metastasis; osteoarthritis;
KW	angiogenic disease; neovascular glaucoma; diabetic retinopathy; therapy;
KW	rheumatoid arthritis; endometriosis; muscular degeneration;
XX	
OS	Homo sapiens.
XX	
PN	W09929861-A1.
PD	17-JUN-1999.
XX	
PF	09-DEC-1998; 98MO-US26103.
XX	
PR	12-DEC-1997; 97US-0069687.
XX	
PI	09-DEC-1997; 97US-0069155.
XX	
XX	(CHIL-) CHILDRENS MEDICAL CENT.
XX	Klagsbrun M, Soker S;
XX	WPI; 1999-385607/32.
XX	

Pt	New peptide antagonists of vascular endothelial growth factor (VEGF)
Px	Claim 1; Page 46,53pp; English.
Cc	This sequence represents a vascular endothelial growth factor (VEGF) antagonist of the invention. The antagonist is a portion of the seventh exon of VEGF, and acts as an antagonist to all VEGF isoforms, even if they do not have exon 7. The VEGF antagonist peptides can be used to treat diseases or disorders associated with VEGF-induced neovascularisation or inappropriate angiogenesis. Diseases and disorders treated include retinal neovascularisation, haemangiomas, solid tumour growth, leukaemia, metastasis, psoriasis, neovascular glaucoma, diabetic retinopathy, rheumatoid arthritis, osteoarthritis, endometriosis, muscular degeneration, and retinopathy of prematurity (ROP), and Kaposi's sarcoma. Solid tumours expressing VEGF are also a target for gene therapy using the peptide antagonist of the invention, e.g. neuroblastoms of the central nervous system (glioblastomas, astrocytomas, neuroblastomas, meningiomas,ependyromas), cancers of hormone-dependent tissues (e.g. prostate, testicles, uterus, ovary, mammary carcinoma), melanomas, cancers of the lung, and cancers of the gastrointestinal tract. Current treatment of angiologenic diseases is inadequate. Although preliminary results with antiangioegenic proteins are promising, the proteins are relatively large in size and so are difficult to use and produce.
Cc	Antiangeoegenic agents that show improvement in size, ease of production, stability and/or potency would be desirable. The peptides of the invention go some way to achieving these aims.
Sq	Sequence 45 AA:
Query Match	100.0%; Score 264; DR 20; Length 45;
Best Local Similarity	100.0%; Pred. NO. 4.9e-22;
Matches 45; Conservative 0; Mismatches 0; Indels 0; Gaps 0	
Gz	1 PGGPCSERRKHLVDDPQTCCKSCAKNTDSRCAKDLELNERTCRC 45 Db 1 pggpcseerrkhlvddpqtcckscakntdsrcaqrqlnerircrc 45
AAR42613	
ID AAR42613 standard; Protein; 44 AA.	
AAR42613;	
Dt 28-OCT-1993 (first entry)	
DE Encoded by human VEGF-165 exon VII.	
Kw Angiogenesis; wound healing; mitogen; vascular endothelial cells; Vascular Endothelial Cell Growth Factor; hVEGF-165; hVEGF-121; alternative RNA splicing. Homo sapiens. US5219739-A. 15-JUN-1993. 27-JUL-1989; 89US-0387545. PF 27-JUL-1989; 89US-0387545. XX 27-JUL-1989; 89US-0387545. PR 14-DEC-1989; 89US-0450883. XX 27-JUL-1990; 90US-0559041. (SCIO-) SCIOS NOVA INC. Abraham JA, Fildes JC, Mitchell RL, Fischer EG, WPI: 1993-205302/25. DR N-PSDB; AAAQ49609. Isolated DNA sequences, expression vectors and transformant cells	

PT	- used for large scale prodn. of vascular endothelial cell growth
PT	factor. for treating wounds in which neo-vascularisation is
PT	required
XX	
PS	Claim 8; Fig 8; 40pp; English.
XX	
CC	The sequences of the 8 possible exons encoding human vascular
CC	endothelial cell growth factor, together with contiguous splice
CC	junctions, were obtained from overlapping genomic inserts. A method
CC	for producing VEGF is claimed comprising culturing mammalian cells
CC	transformed with an expression vector containing exons I-V and
CC	VIII. See AAQ44261 for exon I and AAQ49604-Q49610 for exons II-VIII.
XX	
SO	Sequence 44 AA;
OY	
Db	1 PGGCSERRKHLFVODPOTCGSCKNFTDSRCKAROLELNEETCR 44 1 pggcserrrkhlfvodpgtckscxknftdsrckarqelnercr 44
RESULT	3
ID	AAAY23249
AC	AAAY23249 standard; Protein; 44 AA.
XX	
DT	31-AUG-1999 (first entry)
XX	
DE	SEQ ID NO. 11 of WO9930157.
XX	
KW	Cancer; vascular endothelial growth factor receptor; VEGF receptor; neuropilin; NP-1; NP-2; metastatic potential; malignant cell; breast cancer; prostate cancer; Ischemia; gene therapy; angiogenesis; metastasis.
XX	
OS	Homo sapiens.
XX	
PN	WO9930157-A2.
PD	17-JUN-1999.
XX	
PF	09-DEC-1998; 98WO-US26127.
XX	
PR	12-DEC-1997; 97US-0069687. 09-DEC-1997; 97US-0069155.
PA	(CHIL-) CHILDRENS MEDICAL CENT.
PI	Klagsbrun M, Miao H, Soker S, Takashima S; WPI; 1999-395021/33.
DR	
XX	
PT	Diagnosis and prognosis of cancer using vascular endothelial growth factor receptors
XX	
PS	Disclosure; Page 80; 82pp; English.
CC	The specification describes methods for the diagnosis and prognosis of cancer using vascular endothelial growth factor (VEGF) receptors (neuropilins) such as VEGFR165R/NP-1 and NP-2 which are associated with metastatic potential of a malignant cell. The methods can be used for the diagnosis and prognosis of cancer, especially breast and prostate cancer. DNA encoding VEGFR165R/NP-1 or NP-2 can be used to treat ischemia, e.g. heart and limb. The DNA can also be used as an adjunct to gene therapy with VEGF. The VEGFR165R/NP-1 or NP-2 proteins can be used to identify antagonists and agonists, which can be used to inhibit angiogenesis, and metastasis in malignant cells. Antibodies directed against VEGFR165R/NP-1 or NP-2 proteins can also be used for

CC the treatment or prophylaxis of cancers. The present sequence is
 CC used in the course of the invention.

XX Sequence 44 AA;

Query Match 96.6%; Score 255; DB 20; Length 44;
 Best Local Similarity 100.0%; Pred. No. 4.5e-21;
 Matches 44; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PCGPGSERRRKHLFVDPQTCCKSCKMTDSRCKAROLELNERTC 44
 Db 1 pcgpgserrrkhlfvdpqtcckscskmtdsrckarqlelnertr 44

RESULT 4

AAR94041
 ID - AAR94041 standard; Protein; 44 AA.

XX AAR94041;

DT 10-OCT-1996 (first entry)

XX VEGF exon VII.

XX Vascular endothelial growth factor; VEGF; human; conjugate; tumour; iris;
 KW proliferation inhibition; VEGF-mediated pathophysiological condition;
 KW dermatological disorder; VEGF receptor; vascular proliferation; retina;
 KW ophthalmic disorder; hyperproliferating blood vessel; therapy; psoriasis;
 KW conjunctiva; vitreous humour; rheumatoid arthritis; skin cancer;
 KW varicose veins; gene therapy.

XX Homo sapiens.

XX MO9606641-A1.

PN 07-MAR-1996.

XX 29-AUG-1995; 95WO-US10973.

XX 16-MAY-1995; 95US-0441979.

PR 29-AUG-1994; 94US-0297961.

XX (PRIZ-) PRIZM PHARM INC.

XX Fleurbailf GA, Freund E, Houston LL, Nova MP, Sosnowski BA;

PI Victor KD;

DR WPI; 1996-160151/16.

DR N-PSDB; AAT17749.

XX Vascular endothelial cell growth factor (VEGF) conjugates - having
 PT VEGF linked to targeted agent, used for inhibiting proliferation of
 PT cells, e.g. for gene therapy

XX Disclosure; Page 121; 193pp; English.

XX AAR94033-R94038, AAR94041, AAR94042 and AAM00582 represent vascular
 CC endothelial growth factors (VEGF) exons. This sequence represents exon
 CC VII. These sequences were used in VEGF conjugates of the invention. In
 CC the conjugates, VEGF (or fragments of it) are linked to a targeted agent
 CC (this can be via a linker sequence), so that the conjugate binds to a
 CC VEGF receptor. Cys-modified forms of VEGF are particularly suitable for
 CC chemical conjugation to linkers and targeted agents. The conjugates are
 CC used for inhibiting proliferation of cells bearing VEGF receptors. They
 CC can be used for treating a VEGF-mediated pathophysiological condition,
 CC including dermatological disorders with underlying vascular
 CC proliferation, solid tumours or an ophthalmic disorder of
 CC hyperproliferating blood vessels of the retina, iris, conjunctiva or
 CC vitreous humour. The conjugates can also be used for treating
 CC psoriasis, rheumatoid arthritis, skin cancers and other tumours, or
 CC varicose veins. They are also suitable for use in gene therapy.

SQ Sequence 44 AA;

Query Match 94.7%; Score 250; DB 17; Length 44;
 Best Local Similarity 100.0%; Pred. No. 1.6e-20;
 Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PCGPGSERRRKHLFVDPQTCCKSCKMTDSRCKAROLELNERTC 43
 Db 1 pcgpgserrrkhlfvdpqtcckscskmtdsrckarqlelnertr 43

RESULT 5

AAB18547
 ID AAB18547 standard; peptide; 41 AA.

XX AAB18547;

DT 15-JAN-2001 (first entry)

XX Immunogenic peptide fragment derived from FGF and/or VEGF.

XX Immunogenic peptide; fibroblast growth factor; FGF; VEGF; cancer;
 KW vascular endothelial growth factor; hyperproliferative disorder;
 KW haemangioma; solid tumour; blood borne tumour; leukaemia; metastasis;
 KW telangiectasia; psoriasis; scleroderma; pyogenic granuloma;
 KW myocardial angiogenesis; Crohn's disease; plaque neovascularisation;
 KW arteriovenous malformation; corneal disease; rubecosis;
 KW neovascular glaucoma; diabetic retinopathy; retrolental fibroplasia;
 KW arthritis; diabetic neovascularisation; macular degeneration;
 KW wound healing; peptic ulcer; Helicobacter related disease; fracture;
 KW keloid; vasculogenesis; hematopiesis; ovulation; menstruation;
 KW placentalion; cat scratch fever.

XX Unidentified.

XX WO200053219-A2.

PN 14-SEP-2000.

XX 10-MAR-2000; 2000MO-US06320.

XX 11-MAR-1999; 99US-026543.

XX (ENTR-) ENTREMED INC.

XX Holaday JW, Ruiz A, Madsen J;

PI Holaday JW, Ruiz A, Madsen J;

DR WPI; 2000-594263/56.

XX An immunogenic composition useful for treating cancer or
 PT hyperproliferative disorders comprises an immunogenic peptide fragment
 PT of fibroblast growth factor and/or vascular endothelial growth factor -
 XX Claim 13; Page 28; 95pp; English.

XX AAB18542-51 represent immunogenic peptide fragments of fibroblast
 CC growth factor (FGF) and/or vascular endothelial growth factor (VEGF).
 CC The peptides are used to produce immunogenic compositions. The
 CC immunogenic composition is used for treating cancer or
 CC hyperproliferative disorders, especially haemangioma, solid tumours,
 CC blood borne tumours, leukaemia, metastasis, telangiectasia, psoriasis,
 CC scleroderma, pyogenic granuloma, myocardial angiogenesis, Crohn's
 CC disease, plaque neovascularisation, arteriovenous malformations,
 CC corneal diseases, rubecosis, neovascular glaucoma, diabetic retinopathy,
 CC retrolental fibroplasia, arthritis, diabetic neovascularisation, macular
 CC degeneration, wound healing, peptic ulcer, Helicobacter related
 CC diseases, fractures, keloids, vasculogenesis, hematopolesis, ovulation,
 CC menstruation, placentalion and cat scratch fever.

Query Match 67.4%; Score 178; DB 21; Length 41;
 Best Local Similarity 89.7%; Pred. No. 9.4e-13;
 Matches 35; Conservative 0; Mismatches 0; Indels 4; Caps 2;

OY 7 ERKKLFYQDPQTCCKSKNTDSRCARQLEINERTCRC 45
 Db 2 ertkhlty--qtckscskndsrckarqlenertcrc 36

RESULT 6

AAV22024

ID AAV22024 standard; peptide: 24 AA.

XX AAV22024:

DT 26-AUG-1999 (first entry)

DE VEGF antagonist peptide.

XX VEGF; vascular endothelial growth factor; antagonist; neovascularisation;
 KW angiogenesis; retinal neovascularisation; haemangioma; Kaposi's sarcoma;
 KW solid tumour growth; leukemia; metastasis; psoriasis; osteoarthritis;
 KW angiogenic disease; neovascular glaucoma; diabetic retinopathy; therapy;
 KW rheumatoid arthritis; endometriosis; muscular degeneration;
 KW retinopathy of prematurity.

XX Homo sapiens.

XX W09929861-A1.

XX 17-JUN-1999.

XX 09-DEC-1998; 98WO-US26103.

XX 12-DEC-1997; 97US-0069687.
 PR 09-DEC-1997; 97US-0069155.

XX (CHIL-) CHILDRENS MEDICAL CENT.

XX Klagsbrun M, Soker S;

XX WPI; 1999-385607/32.

XX New peptide antagonists of vascular endothelial growth factor (VEGF)

XX Claim 2; Page 46; 53pp: English.

XX This sequence represents a vascular endothelial growth factor (VEGF)
 CC antagonist of the invention. The antagonist is a portion of the seventh
 CC exon of VEGF, and acts as an antagonist to all VEGF isoforms, even if
 CC they do not have exon 7. The VEGF antagonist peptides can be used to
 CC treat diseases or disorders associated with VEGF-induced
 CC neovascularisation or inappropriate angiogenesis. Diseases and disorders
 CC treated include retinal neovascularisation, haemangiomas, solid tumour
 CC growth, leukaemia, metastasis, psoriasis, neovascular glaucoma, diabetic
 CC retinopathy, rheumatoid arthritis, osteoarthritis, endometriosis,
 CC muscular degeneration, and retinopathy of prematurity (ROP), and Kaposi's
 CC sarcoma. Solid tumours expressing VEGF are also a target for gene
 CC therapy using the peptide antagonist of the invention, e.g. neoplasms of
 CC the central nervous system (glioblastomas, astrocytomas, neuroblastomas,
 CC meningiomas, ependymomas), cancers of hormone-dependent tissues (e.g.
 CC prostate, testicles, uterus, ovary, mammary carcinoma), melanomas,
 CC cancers of the lung, and cancers of the gastrointestinal tract. Current
 CC treatment of angiogenic diseases is inadequate. Although preliminary
 CC results with antiangiogenic proteins are promising, the proteins are
 CC relatively large in size and so are difficult to use and produce.
 CC Antiangiogenic agents that show improvement in size, ease of production,
 CC stability and/or potency would be desirable. The peptides of the
 CC invention go some way to achieving these aims.

SQ Sequence 24 AA;

Query Match 52.3%; Score 138; DB 20; Length 24;
 Best Local Similarity 100.0%; Pred. No. 1.3e-08;
 Matches 24; Conservative 0; Mismatches 0; Indels 0; Caps 0;

OY 22 CSCKNTDSRCARQLEINERTCRC 45
 Db 1 cskntdsrckarqlenertcrc 24

RESULT 7

AAV22025

ID AAV22025 standard; peptide: 21 AA.

XX AAV22025:

DT 26-AUG-1999 (first entry)

DE VEGF antagonist peptide.

XX VEGF; vascular endothelial growth factor; antagonist; neovascularisation;
 KW angiogenesis; retinal neovascularisation; haemangioma; Kaposi's sarcoma;
 KW solid tumour growth; leukemia; metastasis; psoriasis; osteoarthritis;
 KW angiogenic disease; neovascular glaucoma; diabetic retinopathy; therapy;
 KW rheumatoid arthritis; endometriosis; muscular degeneration;
 KW retinopathy of prematurity.

XX Homo sapiens.

XX W09929861-A1.

XX 17-JUN-1999.

XX 09-DEC-1998; 98WO-US26103.

XX 12-DEC-1997; 97US-0069687.
 PR 09-DEC-1997; 97US-0069155.

XX (CHIL-) CHILDRENS MEDICAL CENT.

XX Klagsbrun M, Soker S;

XX WPI; 1999-385607/32.

XX New peptide antagonists of vascular endothelial growth factor (VEGF)

XX Claim 3; Page 46; 53pp: English.

XX This sequence represents a vascular endothelial growth factor (VEGF)
 CC antagonist of the invention. The antagonist is a portion of the seventh
 CC exon of VEGF, and acts as an antagonist to all VEGF isoforms, even if
 CC they do not have exon 7. The VEGF antagonist peptides can be used to
 CC treat diseases or disorders associated with VEGF-induced
 CC neovascularisation or inappropriate angiogenesis. Diseases and disorders
 CC treated include retinal neovascularisation, haemangiomas, solid tumour
 CC growth, leukaemia, metastasis, psoriasis, neovascular glaucoma, diabetic
 CC retinopathy, rheumatoid arthritis, osteoarthritis, endometriosis,
 CC muscular degeneration, and retinopathy of prematurity (ROP), and Kaposi's
 CC sarcoma. Solid tumours expressing VEGF are also a target for gene
 CC therapy using the peptide antagonist of the invention, e.g. neoplasms of
 CC the central nervous system (glioblastomas, astrocytomas, neuroblastomas,
 CC meningiomas, ependymomas), cancers of hormone-dependent tissues (e.g.
 CC prostate, testicles, uterus, ovary, mammary carcinoma), melanomas,
 CC cancers of the lung, and cancers of the gastrointestinal tract. Current
 CC treatment of angiogenic diseases is inadequate. Although preliminary
 CC results with antiangiogenic proteins are promising, the proteins are
 CC relatively large in size and so are difficult to use and produce.
 CC Antiangiogenic agents that show improvement in size, ease of production,
 CC stability and/or potency would be desirable. The peptides of the
 CC invention go some way to achieving these aims.

SQ Sequence 21 AA;

Db 9 cpctgtgrgr---pdrtrcrtrrrrrflhcgqgylepnptc 50

RESULT 10

AAR36680

ID AAR36680 standard; peptide; 20 AA.

XX AAR36680;

XX 23-AUG-1993 (first entry)

XX Guinea pig VPF C-terminal.

XX Vascular permeability factor; effusion; malignancy; antibody;

XX guinea pig; human.

XX Cavia porcellus.

XX WO9308473-A.

XX 29-APR-1993.

XX 21-OCT-1992; 92WO-US09068.

XX 24-OCT-1991; 91US-0782350.

XX (BETH-) BETH ISRAEL HOSPITAL ASSOC.

XX Dvorak HF, Yeo K, Yeo T;

XX WPI; 1993-152625/18.

XX Immunassay for detecting vascular permeability (VPF) factor in

XX effusions - comprises detecting VPF in sample using immobilised

XX antibody to C-terminus of VPF having specified sequence and 2nd

XX labelled antibody to N-terminus

XX Claim 8; Page 20; 33pp; English.

XX An assay method for determining whether an effusion sample obtd.

XX from a human patient is associated with a malignancy, comprises

XX measuring VPF in the sample, a VPF level greater than a

XX predetermined amts. Indicates a likelihood that the sample is a

XX malignant effusion. More specifically, the assay is carried out

XX with an immobilised first antibody to the C-terminus of guinea pig

XX VPF (AAR36680) and a second labelled antibody to the N-terminus of

XX human VPF (AAR36679). The label is pref. a Europium chelate. A level

XX of more than 30 units indicates a malignant effusion.

XX Sequence 20 AA;

Query Match

ID AAG08910

XX AAG08910;

XX 17-OCT-2000 (first entry)

XX Arabidopsis thaliana protein fragment SEQ ID NO: 6631.

XX Protein identification; signal transduction pathway; metabolic pathway;

KW hybridisation assay; genetic mapping; gene expression control; promoter;
XX termination sequence.

XX Arabidopsis thaliana.

XX EP1033405-A2.

XX 06-SEP-2000.

XX 25-FEB-2000; 2000EP-0301439.

XX 25-FEB-1999; 99US-0121825.

XX 05-MAR-1999; 99US-0123180.

XX 09-MAR-1999; 99US-0123548.

XX 23-MAR-1999; 99US-0125788.

XX 25-MAR-1999; 99US-0126264.

XX 29-MAR-1999; 99US-0126785.

XX 01-APR-1999; 99US-0127462.

XX 06-APR-1999; 99US-0128234.

XX 08-APR-1999; 99US-0128714.

XX 16-APR-1999; 99US-0129845.

XX 19-APR-1999; 99US-0130077.

XX 21-APR-1999; 99US-0130449.

XX 23-APR-1999; 99US-0130510.

XX 28-APR-1999; 99US-0130891.

XX 30-APR-1999; 99US-0131449.

XX 04-MAY-1999; 99US-0132048.

XX 05-MAY-1999; 99US-0132484.

XX 06-MAY-1999; 99US-0132485.

XX 06-MAY-1999; 99US-0132486.

XX 07-MAY-1999; 99US-0132487.

XX 11-MAY-1999; 99US-0132863.

XX 14-MAY-1999; 99US-0134256.

XX 14-MAY-1999; 99US-0134219.

XX 14-MAY-1999; 99US-0134221.

XX 14-MAY-1999; 99US-0134370.

XX 18-MAY-1999; 99US-0134768.

XX 19-MAY-1999; 99US-0134941.

XX 20-MAY-1999; 99US-0135124.

XX 21-MAY-1999; 99US-0135353.

XX 24-MAY-1999; 99US-0135629.

XX 25-MAY-1999; 99US-0136021.

XX 27-MAY-1999; 99US-0136392.

XX 28-MAY-1999; 99US-0136782.

XX 01-JUN-1999; 99US-0137222.

XX 03-JUN-1999; 99US-0137528.

XX 04-JUN-1999; 99US-0137502.

XX 07-JUN-1999; 99US-0137724.

XX 08-JUN-1999; 99US-0138094.

XX 10-JUN-1999; 99US-0138540.

XX 10-JUN-1999; 99US-0138847.

XX 14-JUN-1999; 99US-0139119.

XX 16-JUN-1999; 99US-0139452.

XX 16-JUN-1999; 99US-0139453.

XX 17-JUN-1999; 99US-0139492.

XX 18-JUN-1999; 99US-0139454.

XX 18-JUN-1999; 99US-0139455.

XX 18-JUN-1999; 99US-0139456.

XX 18-JUN-1999; 99US-0139457.

XX 18-JUN-1999; 99US-0139458.

XX 18-JUN-1999; 99US-0139459.

XX 18-JUN-1999; 99US-0139460.

XX 18-JUN-1999; 99US-0139461.

XX 18-JUN-1999; 99US-0139462.

XX 18-JUN-1999; 99US-0139463.

XX 18-JUN-1999; 99US-0139470.

XX 18-JUN-1999; 99US-0139750.

XX 21-JUN-1999; 99US-0139763.

XX 22-JUN-1999; 99US-0139817.

XX 23-JUN-1999; 99US-0139899.

XX 23-JUN-1999; 99US-0140353.

XX 23-JUN-1999; 99US-0140354.

PD 06-SEP-2000.
XX
XX 25-FEB-2000; 2000EP-0301439.
XX
PR 25-FEB-1999; 99US-0121825.
PR 05-MAR-1999; 99US-0123180.
PR 09-MAR-1999; 99US-0123548.
PR 23-MAR-1999; 99US-0125788.
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AC AAG05269;

XX 17-OCT-2000 (first entry)

DE Arabidopsis thaliana protein fragment SEQ ID NO: 1611.

KW Protein identification; signal transduction pathway; metabolic pathway;
KW hybridisation assay; genetic mapping; gene expression control; promoter;
KW termination sequence.

XX Arabidopsis thaliana.

XX EP1033405-A2.

XX 06-SEP-2000.

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DE Arabidopsis thaliana protein fragment SEQ ID NO: 6630.
XX Protein identification: signal transduction pathway; metabolic pathway;
KW hybridisation assay; genetic mapping; gene expression control; promoter;
KW termination sequence.
XX Arabidopsis thaliana.
OS Arabidopsis thaliana.
XX EP1033405-A2.
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PR 29-OCT-1999; 99US-0162142.

Query Match 22.0%; Score 58; DB 21; Length 67;
Best Local Similarity 39.0%; Pred. No. 15;
Matches 16; Conservative 4; Mismatches 17; Indels 4; Gaps 2;

QY 7 ERKHLFVODPQTCKSCGKNTDSCKAROLELNERTC--RC 45
Db 7 eyrvellnklaqtcfknc--vdkrykeaelmgenscdirc 45

RESULT 15

AG43389
ID AG43389 standard; Protein: 67 AA.

AC AAG43389;

DT 18-OCT-2000 (first entry)

DE Arabidopsis thaliana protein fragment SEQ ID NO: 54226.

KM Protein identification; signal transduction pathway; metabolic pathway;
hybridisation assay; genetic mapping; gene expression control; promoter;
termination sequence.

OS Arabidopsis thaliana.

PN EP1033405-A2.

PD 06-SEP-2000.

PF 25-FEB-2000; 2000EP-0301439.

PR 25-FEB-1999; 99US-0121825.

PR 05-MAR-1999; 99US-0123180.

PR 09-MAR-1999; 99US-0123548.

PR 23-MAR-1999; 99US-0125788.

PR 25-MAR-1999; 99US-0126264.

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PR 28-OCT-1999; 99US-0161992.
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PR 29-OCT-1999; 99US-0162142.

Query Match 22.0%; Score 58; DB 21; Length 67;
Best Local Similarity 39.0%; Pred. No. 15;
Matches 16; Conservative 4; Mismatches 17; Indels 4; Gaps 2;

QY 7 ERKKHLFVODPQCCKSCCKNTDSCRKAROLELNERTC--RC 45
Db 7 eyrvellnklaqlctfkc--vdkrykeaelmgenscidrc 45

Search completed: January 31, 2002, 11:21:08
Job time: 309 sec

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GenCore version 4.5
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OM protein - protein search, using sw model

Run on: January 31, 2002, 11:20:19 ; Search time 21.83 Seconds
(without alignments)
301.523 Million cell updates/sec

Title: US-09-579-420-1

Perfect score: 264
Sequence: 1 PCGPCSRRRKHLFVQDPQC.....NTDSRCKAROLEINERTCRC 45

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 473505 seqs, 146272329 residues

Total number of hits satisfying chosen parameters: 92817

Minimum DB seq length: 0
Maximum DB seq length: 100

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

SPTREMBL_17:*
1: sp-archaea:*
2: sp-bacteria:*
3: sp-fungi:*
4: sp-human:*
5: sp_invertebrate:*
6: sp-mammal:*
7: sp-mhc:*
8: sp-organelle:*
9: sp-phage:*
10: sp-plant:*
11: sp-rodent:*
12: sp-virus:*
13: sp-vertebrate:*
14: sp_unclassified:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	59.5	22.5	77	5	Q23771 chironomus
2	54.5	20.6	72	12	Q23803 chironomus
3	54.5	20.6	72	12	Q75533 human immun
4	53	20.1	43	5	Q9VDN2 drosophila
5	53	20.1	43	5	Q9VM82 drosophila
6	52	19.7	81	10	Q9AVE2 arabidopsis
7	51.5	19.5	83	5	Q23783 chironomus
8	51	19.3	71	10	Q9LRE0 brassica ca
9	49.5	18.8	72	12	Q98XG2 human immun
10	49.5	18.8	72	12	Q9A1S8 chlamydomon
11	48.5	18.4	98	2	Q48496 bacterioph
12	48.5	18.4	99	5	Q9N329 caenorhabd
13	48	18.2	61	2	Q9ZHI9 desulfofoma
14	48	18.2	66	5	Q9VEI4 drosophila
15	48	18.2	81	10	Q82789 brassica o1
16	48	18.2	88	2	P94663 chlamydia p
17	47.5	18.0	60	6	Q9TS92 bos taurus
18	47.5	18.0	92	2	Q9XIL9 thermotoga
19	47	17.8	42	6	Q46620 equus asinu

20	47	17.8	59	5	P82107 hiru
21	47	17.8	84	13	Q90248 bom
22	46.5	17.6	68	4	Q9UE57 homo sapien
23	46.5	17.6	72	12	Q75531 human immun
24	46.5	17.6	72	12	Q75529 human immun
25	46.5	17.6	72	12	Q75530 human immun
26	46.5	17.6	72	12	Q75532 human immun
27	46.5	17.6	72	12	Q75537 human immun
28	46.5	17.6	72	12	Q75538 human immun
29	46.5	17.6	95	5	Q23723 chironomus
30	46	17.4	48	6	P79380 sus scrofa
31	46	17.4	68	6	Q9N139 bos taurus
32	46	17.4	70	2	Q34083 streptococ
33	46	17.4	73	5	Q62554 mytilus edu
34	46	17.4	76	11	Q70556 mus musculu
35	46	17.4	98	12	Q9XRI9 human cytom
36	45.5	17.2	62	6	Q9TUI5 canis fami
37	45.5	17.2	86	10	Q989M3 arabidopsi
38	45.5	17.2	100	5	P90911 caenorhabd
39	45	17.0	48	2	Q9RFP5 mycoplasma
40	45	17.0	72	5	Q9VZQ4 drosophila
41	45	17.0	76	11	Q70557 mus musculu
42	45	17.0	78	10	Q9S9H8 vigna ungui
43	45	17.0	79	10	Q9MB54 brassica ca
44	45	17.0	84	10	Q9XH47 pinus taeda
45	45	17.0	89	12	Q69699 human immun

ALIGNMENTS

RESULT 1	Q23771	PRELIMINARY;	PRT;	77 AA.
ID	Q23771;			
AC	Q23771;			
DT	01-NOV-1996 (TREMBlrel. 01, Created)			
DT	01-NOV-1996 (TREMBlrel. 01, Last sequence update)			
DT	01-NOV-1996 (TREMBlrel. 01, Last annotation update)			
DE	BALBANI RING (BRI), SECRETORY PROTEIN SP-1A REPETITIVE REGION (FRAGMENT).			
OS	Chironomus pallidivittatus (Midge).			
OC	Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;			
OC	Pterygota; Neoptera; Endopterygota; Diptera; Nematocera;			
OC	Chironomidae; Chironomidae; Chironomidae; Chironomus.			
NO	NCBI_TaxID=7151;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RA	Galler R., Rydlander L., Riedel N., Kluding H., Edstroem J.E.;			
RL	Proc. Natl. Acad. Sci. U.S.A. 81:1448-1452(1984).			
DR	EMBL; K01693; AAA28237.1; -			
FT	NON_TER 1			
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SQ	SEQUENCE 77 AA; 8513 MW; P498E7D5DCB02A38 CRC64;			
Query Match	22.5%; Score 59.5; DB 5; Length 77;			
Best Local Similarity	33.3%; Pred. No. 0.64; Mismatches 10; Conservative 7; Indels 1; Gaps 1;			
Matches	10; Conservative 7; Indels 1; Gaps 1;			
QY	17 PCPCGSCCKNTD-SRCKAROLEINERTCRC 45			
DB	2 PCPCGSMRRVEGRCARARGRFNDKNCRC 31			
RESULT 2	Q23803	PRELIMINARY;	PRT;	63 AA.
ID	Q23803;			
AC	Q23803;			
DT	01-NOV-1996 (TREMBlrel. 01, Created)			
DT	01-JAN-1999 (TREMBlrel. 09, Last sequence update)			
DT	01-JAN-1999 (TREMBlrel. 09, Last annotation update)			
DE	185-KDA SECRETORY PROTEIN (SPI85) (FRAGMENT).			
OS	Chironomus tentans (Midge).			

OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
 OC Pterygota; Neoptera; Endopterygota; Diptera; Nematocera;
 OC Chironomidae; Chironomidae; Chironominae; Chironomus.
 OX NCBI_TaxID=7153;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=89255447; PubMed=2470756;
 RA Dignam S.S., Yang L., Iezzi M., Case S.T.;
 RT "Identification of a developmentally regulated gene for a 140-kDa
 RT secretory protein in salivary glands of Chironomus tentans larvae."
 RL J. Biol. Chem. 264:9444-9452(1989).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=90269600; PubMed=2189782;
 RA Dignam S.S., Case S.T.;
 RT "Baldian ring 3 in Chironomus tentans encodes a 185-kDa secretory
 RT protein which is synthesized throughout the fourth larval instar."
 RL Gene 88:133-140(1990).
 DR EMBL: M24160; AAA28263.1; -.
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 FT 63 63
 SO SEQUENCE 63 AA; 6963 MW; 1C8BF8CA3486F5CE CRC64;

Query Match 20.6%; Score 54.5; DB 5; Length 63;
 Best Local Similarity 34.6%; Pred. No. 2.6;
 Matches 9; Conservative 4; Mismatches 12; Indels 1; Gaps 1;

OY 20 CXCCKNTDSCRKAROLELNERTCRC 45
 Db 14 CICECTTPATCEGKQTWCE-ACQC 38

RESULT 3
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 AC 075533;
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 DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
 DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
 DE ENVELOPE GLYCOPROTEIN (FRAGMENT).
 GN ENV.
 OS Human immunodeficiency virus type 1.
 OC Viruses; Retrovirdae; Lentivirus.
 OX NCBI_TaxID=11676;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=704A.
 RA Lorenzo E., Herrera R.J., Lai S., Fischl M.A., Hill M.D.;
 RL Submitted (May-1996) to the EMBL/GenBank/DBJ databases.
 DR EMBL: U57241; AAB17801.1; -.
 DR InterPro: IPR001831; HIV_Tat.
 DR Pfam: PF00539; Tat; 1
 DR PRINTS; PR00055; HIVTATDOMAIN.
 KW Envelope protein.
 FT NON_TER 1 1
 FT 72 72
 SO SEQUENCE 72 AA; 8333 MW; 6877B110FB082120 CRC64;

Query Match 20.6%; Score 54.5; DB 12; Length 72;
 Best Local Similarity 41.2%; Pred. No. 2.9;
 Matches 14; Conservative 1; Mismatches 18; Indels 1; Gaps 1;

OY 1 PCGPCSERKHLFVODPQC-KCCKNTDSCRA 33
 Db 3 PYDRLERKHPGSOPTACTKCYCKKCPHQA 36

RESULT 4
 09VDN2 PRELIMINARY; PRT; 43 AA.
 AC 09VDN2;

DT 01-MAY-2000 (TrEMBLrel. 13, Created)
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
 DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
 DE CG5097 PROTEIN.
 GN CG5097.
 OS Drosophila melanogaster (Fruit fly).
 OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
 OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 OC Ephydroidea; Drosophilidae; Drosophila.
 OX NCBI_TaxID=7227;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=BERKELEY;
 RX MEDLINE=20196006; PubMed=10731132;
 RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
 RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
 RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
 RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
 RA Brandon R.C., Rogers Y.-H.C., Blazer G., Champe M., Pfeiffer B.D.,
 RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Milos G.L.G.,
 RA Abril J.F., Aghayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
 RA Ballieu R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
 RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
 RA Borokova D., Botchan M.R., Bouck J., Brokstein P., Brotlier P.,
 RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
 RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
 RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
 RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
 RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
 RA Foster C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
 RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
 RA Harris N.L., Harvey D., Helman T.J., Hernandez J.R., Houck J.,
 RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
 RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
 RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
 RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
 RA Liu X., Matel B., McIntosh T.C., McLeod M.P., McPherson D.,
 RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
 RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
 RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pauley J.M.,
 RA Palazolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
 RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
 RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
 RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
 RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
 RA Wang Z.-Y., Wassarman D.A., Weinstein G.M., Weisenbach J.,
 RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
 RA Ye J., Yen R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
 RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
 RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
 RT "The genome sequence of Drosophila melanogaster.";
 RL Science 287:2185-2195(2000).
 DR EMBL: AE003730; AAP55758.1; -.
 DR FLYbase: FBgn0038790; CG5097.
 DR InterPro: IPR000561; EGF-like.
 DR InterPro: IPR000966; Melittin-like.
 DR Pfam: PF02067; Melittin-like.
 DR PRINTS; PR00872; MTDIPTERA.
 DR PROSITE; PS00022; EGF_1; UNKNOWN_1.
 SO SEQUENCE 43 AA; 4597 MW; E54E722B14EB9DFE CRC64;

Query Match 20.1%; Score 53; DB 5; Length 43;
 Best Local Similarity 52.6%; Pred. No. 3.1;
 Matches 10; Conservative 2; Mismatches 5; Indels 2; Gaps 1;

OY 18 QTCCKCKN--TDSRCKA 34
 Db 25 QDCKCVCCKNGPKDCKSK 43

RESULT 5
 09VM82


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ID 09VW82 PRELIMINARY: PRT: 45 AA.
AC 09VW82;
DT 01-MAY-2000 (Tremblrel. 13, Created)
DT 01-MAY-2000 (Tremblrel. 13, Last sequence update)
DT 01-MAR-2001 (Tremblrel. 16, Last annotation update)
DE CG18461 PROTEIN.
GN CG17376 OR CG18461.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OC NCBI_Taxid=7227;
RN (1)
RP SEQUENCE FROM N.A.
RC STRAIN=BERKELEY;
RX MEDLINE=20196006; PubMed=10731132;
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Mortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.-H.C., Blazel R.G., Champe M., Pfeiffer B.D.,
RA Man K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA Abril J.F., Aghayani A., An H.-J., Andrews-Frankoch C., Baldwin D.,
RA Ballew R.M., Basu A.V., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brotlier P.,
RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahike C., Dayenport L.B., Davies P.,
RA de Pablo B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
RA Foster C., Gabriellian A.E., Gary N.S., Gelbart W.M., Glasser K.,
RA Glodok A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegam C.,
RA Jalali M., Kalush F., Kapen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Merkulov G., Mishina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Nelson D.R., Nelson K.A., Nixon K., Nuskern D.R., Pacleb J.M.,
RA Palazolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Switzkas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Wang Z.-Y., Wasserman D.A., Weinstein G.M., Weissenbach J.,
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RT "The genome sequence of Drosophila melanogaster."
RL Science 287:2185-2195(2000).
DR EMBL; AE003615; AAF52441.1; -
DR Flybase; FBgn0042189; CG17376.
SQ SEQUENCE 45 AA; 4869 MW; F8F92B3B3FB88254 CRC64;

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Query Match 20.1%; Score 53; DB 5; Length 45;
Best Local Similarity 33.3%; Pred. No. 3.2;
Matches 12; Conservative 4; Mismatches 14; Indels 6; Gaps 1;

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OY 2 CGPSERRKHLFVODP-----OTCKCKNTDSRC 31
   ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 8 CGPSPCRRLVKNAPCVCAPCKAHCTNTPPKC 43

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RESULT 6
O9AVE2 PRELIMINARY: PRT: 81 AA.
ID O9AVE2;
AC O9AVE2;
DT 01-JUN-2001 (Tremblrel. 17, Created)

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DT 01-JUN-2001 (Tremblrel. 17, Last sequence update)
DT 01-JUN-2001 (Tremblrel. 17, Last annotation update)
DE SCRB.
OS Arabidopsis lyrata.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids II; Brassicales; Brassicaceae; Arabidopsis.
OC NCBI_Taxid=59689;
RN (1)
RP SEQUENCE FROM N.A.
RX MEDLINE=21149876; PubMed=11251101;
RA Kusaba M., Dwyer K., Hendershot J., Vrebalov J., Nasrallah J.B.,
RA Nasrallah M.E.;
RT "Self-incompatibility in the Genus Arabidopsis: Characterization of
RT the S locus in the outcrossing A. lyrata and its Autogamous Relative
RT A. thaliana."
RL Plant Cell 13:627-643(2001).
DR EMBL; AB052754; BAB40985.1; -
SQ SEQUENCE 81 AA; 9457 MW; 6AAE5C7FB24D291C CRC64;

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Query Match 19.7%; Score 52; DB 10; Length 81;
Best Local Similarity 31.2%; Pred. No. 7;
Matches 15; Conservative 3; Mismatches 20; Indels 10; Gaps 2;

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OY 1 PCGPSERRKHLFVODPOTCKSCSKN---TDSRCKAROLELNTERTC 45
   ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 38 PTPGCGNGE-----ETCKKOPKNITRPPICQCLDKXDFARLDC 78

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RESULT 7
ID 023783 PRELIMINARY: PRT: 83 AA.
AC 023783;
DT 01-NOV-1996 (Tremblrel. 01, Created)
DT 01-NOV-1996 (Tremblrel. 01, Last sequence update)
DT 01-NOV-1998 (Tremblrel. 08, Last annotation update)
DE BALBIANI RING C REPEAT UNIT (FRAGMENT).
OS Chironomus thummi thummi (Midge).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Diptera; Nematocera;
OC Chironomidae; Chironomidae; Chironominae; Chironomus.
OC NCBI_Taxid=7155;
RN (1)
RP SEQUENCE FROM N.A.
RX MEDLINE=84236027; PubMed=7188354;
RA Baumelein H., Wobus U., Gerbi S., Kafatos F.C.;
RT "Characterization of a 249-bp tandemly repetitive, satellite-like
RT repeat in the translated portion of Balbiani ring c of Chironomus
RT thummi."
RL EMBO J. 1:641-647(1982).
DR EMBL; X01859; CAA25979.1; -
FT NON_TER 1
FT NON_TER 83
FT SEQUENCE 83 AA; 8772 MW; 5EE3B8B0B9D04F6 CRC64;
SQ SEQUENCE 83 AA; 8772 MW; 5EE3B8B0B9D04F6 CRC64;

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Query Match 19.5%; Score 51.5; DB 5; Length 83;
Best Local Similarity 22.7%; Pred. No. 8.3;
Matches 10; Conservative 10; Mismatches 23; Indels 1; Gaps 1;

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OY 3 GCPSERRKHLFVODPOTCKCKNTDS-RCAROLELNTERTC 45
   ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 32 GPKTSKSGKPKPKPEKGSAMKRTKAKKNGRNSKRC 75

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RESULT 8
O9LREO PRELIMINARY: PRT: 71 AA.
ID O9LREO;
AC O9LREO;
DT 01-OCT-2000 (Tremblrel. 15, Created)
DT 01-OCT-2000 (Tremblrel. 15, Last sequence update)

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DT 01-MAR-2001 (TReMBLrel. 16, Last annotation update)
 DE S LOCUS PROTEIN 11-32 (FRAGMENT).
 GN SP11-32.
 OS Brassica campestris (Field mustard).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
 OC eurosids II; Brassicales; Brassicaceae; Brassica.
 NC NCBI_TaxID=3711;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=S32(50-11T);
 RX MEDLINE=20273842; PubMed=10812061;
 RA Matanabe M., Ito A., Takada Y., Ninomiya C., Kakizaki T., Takahata Y.,
 RA Hatakeyama K., Hinata K., Suzuki G., Takasaki T., Satta Y., Shiba H.,
 RA Takayama S., Isogai A.;
 RT "Highly divergent sequences of the pollen self-incompatibility (S)
 RT gene in class-I S haplotypes of Brassica campestris (syn. rapa) L.";
 RL FEBS Lett. 473:139-144(2000).
 DR EMBL: AB039756; BAA96394.1; -;
 FT NON_TER 1
 SQ SEQUENCE 71 AA; 7928 MW; 1E8E5E88D8720F97 CRC64;

Query Match 19.3%; Score 51; DB 10; Length 71;
 Best Local Similarity 29.0%; Pred. No. 8.6;
 Matches 9; Conservative 5; Mismatches 7; Indels 10; Gaps 1;

OY 15 ODPOTCKSCKNTDSCKARQLELNEPTC 45
 DB 47 KDPALCSCICRHHBGR-----RFPCC 67

RESULT 9
 O98XG2
 ID O98XG2 PRELIMINARY; PRT; 72 AA.
 AC O98XG2;
 DT 01-JUN-2001 (TReMBLrel. 17, Created)
 DT 01-JUN-2001 (TReMBLrel. 17, Last sequence update)
 DE 01-JUN-2001 (TReMBLrel. 17, Last annotation update)
 DE TAT PROTEIN (FRAGMENT).
 GN TAT.
 OS Human immunodeficiency virus type 1.
 OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
 NC NCBI_TaxID=11676;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=PAIR C MOTHER;
 RA Huisain M., Hahn T., Yedavalli V.R.K., Ahmad N.;
 RT "Molecular Characterization of HIV Type 1 tat Gene from Mother-Infant
 RT Isolates Associated with Perinatal Transmission.";
 RL Submitted (AUG-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AY007033; AAG32897.1; -;
 FT NON_TER 72
 SQ SEQUENCE 72 AA; 8225 MW; B716DB42042D5D46 CRC64;

Query Match 18.8%; Score 49.5; DB 12; Length 72;
 Best Local Similarity 39.4%; Pred. No. 14;
 Matches 13; Conservative 1; Mismatches 18; Indels 1; Gaps 1;

OY 1 PCGPCSERRKHLFYQDPOTC-KCSCKNTDSRCK 32
 DB 3 PVDPRLEPRKHPGSPQTKACKCYKACMHCQ 35

RESULT 10
 O9A1S8 PRELIMINARY; PRT; 87 AA.
 AC O9A1S8;
 DT 01-JUN-2001 (TReMBLrel. 17, Created)
 DT 01-JUN-2001 (TReMBLrel. 17, Last sequence update)
 DT 01-JUN-2001 (TReMBLrel. 17, Last annotation update)
 DE SMALL CYSTEINE-RICH OUTER MEMBRANE LIPOPROTEIN.

GN OMLA.
 OS Chlamydomophila abortus.
 OC Bacteria; Chlamydiales; Chlamydiaceae; Chlamydomophila.
 NC NCBI_TaxID=83555;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=EBA;
 RX MEDLINE=21078680; PubMed=11211261;
 RA Bush R.M., Everett K.D.;
 RT "Molecular evolution of the Chlamydiaceae.";
 RL Int. J. Syst. Evol. Microbiol. 51:203-220(2001).
 DR EMBL: AF240773; AAG60549.1; -;
 KW Lipoprotein.
 SQ SEQUENCE 87 AA; 8972 MW; F6DB1E88DAF57D80 CRC64;

Query Match 18.8%; Score 49.5; DB 2; Length 87;
 Best Local Similarity 24.5%; Pred. No. 16;
 Matches 13; Conservative 4; Mismatches 13; Indels 23; Gaps 2;

OY 1 PCGPCSERRKHLFYQDPOTCKSCKNTDSRCK 32
 DB 36 PCNPGCKKKDKGCSPCCTTTPSCTKPCGSECNSSGVGPOA--KGTSLDGRCK 86

RESULT 11
 O48496
 ID O48496 PRELIMINARY; PRT; 98 AA.
 AC O48496;
 DT 01-JUN-1998 (TReMBLrel. 06, Created)
 DT 01-JUN-1998 (TReMBLrel. 06, Last sequence update)
 DT 01-AUG-1998 (TReMBLrel. 07, Last annotation update)
 DE COMPLETE NUCLEOTIDE SEQUENCE.
 OS Bacteriophage SPPL.
 OC Viruses; dsDNA viruses, no RNA stage; Tailed phages; Siphoviridae;
 OC Lambda phage group.
 NC NCBI_TaxID=10724;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Alonso J.C., Luder G., Stiege A.C., Chai S., Weise F., Trautner T.A.;
 RL Submitted (MAY-1996) to the EMBL/GenBank/DBJ databases.
 DR EMBL: X97918; CAA6503.1; -;
 SQ SEQUENCE 98 AA; 10724 MW; EC648DF58CAF7BEF CRC64;

Query Match 18.4%; Score 48.5; DB 9; Length 98;
 Best Local Similarity 34.1%; Pred. No. 24;
 Matches 15; Conservative 3; Mismatches 23; Indels 3; Gaps 1;

OY 2 CGPCSEERRKHLFYQDPOTCKSCKNTDSCKARQLELNEPTC 45
 DB 11 CGPVPVSKKKSINKVEHR---ACKLDSDIVKPMSPRLNERVGR 51

RESULT 12
 O9N329 PRELIMINARY; PRT; 99 AA.
 AC O9N329;
 DT 01-OCT-2000 (TReMBLrel. 15, Created)
 DT 01-OCT-2000 (TReMBLrel. 15, Last sequence update)
 DT 01-OCT-2000 (TReMBLrel. 15, Last annotation update)
 DE HYPOTHETICAL PROTEIN Y59E9AL.5.
 GN Y59E9AL.5.
 OS Caenorhabditis elegans.
 OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidae;
 OC Rhabditidae; Peloderinae; Caenorhabditis.
 NC NCBI_TaxID=6239;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=BRISTOL N2;
 RX MEDLINE=99069613; PubMed=9851916;
 RA None;
 RT "Genome sequence of the nematode C. elegans: a platform for

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RT Investigating biology "The C. elegans Sequencing Consortium.";
RL Science 282:2012-2018(1998).
RN [12]
RP SEQUENCE FROM N.A.
RC STRAIN-BRISTOL N2;
RA Waterston R.;
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AC024838; AAF60819.1;
SQ SEQUENCE 99 AA; 11325 MW; EB3CCC5BFB7DAECC CRC64;

Query Match 18.4%; Score 48.5; DB 5; Length 99;
Best Local Similarity 37.8%; Pred. No. 25;
Matches 14; Conservative 3; Mismatches 13; Indels 7; Gaps 2;

OY 2 CGPCSERRK-----HLFVDDP-QTCCKSCKNMTDSRC 31
| | | | | | | | | | | | | | | | | | | | |
Db: 51 CCACWMRRKKESTTKVCVDDCTCTCSASRCSRC 87

RESULT 13
O92H19 PRELIMINARY; PRT; 61 AA.
AC O92H19;
DT 01-MAY-1999 (TREMBlrel. 10, Created)
DT 01-MAY-1999 (TREMBlrel. 10, Last sequence update)
DT 01-JUN-2001 (TREMBlrel. 17, Last annotation update)
DE FERREDOXIN.
GN FDH.
OS Desulfotomaculum thermocisternum.
OC Bacteria; Firmicutes; Bacillus/Clostridium group; Desulfotomaculum.
OX NCBI_TaxID=42471;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-SF90;
RA Larsen O., Lien T., Birkeland N.-K.;
RT "Dissimilatory sulfite reductase from Archaeoglobus profundus and
RT Desulfotomaculum thermocisternum: phylogenetic and structural
RT implications from gene sequences.";
RL Extremophiles 0:0-0(1999).
DR EMBL; AF074396; AAC96106.1;
DR HSSP; P46797; 1ROR.
DR Interpro; IPR001080; 3FE4S_ferrixdn.
DR Interpro; IPR001450; 4FE4S_ferrixdn.
DR Pfam; PF00037; fer4; 2.
DR PRINTS; PR00352; 3FE4SFEROXIN.
DR PROSITE; PS00196; 4FE4S_FERREDOXIN; 2.
KW Iron-sulfur.
SQ SEQUENCE 61 AA; 6408 MW; EIDF4EAF6F95CAAC CRC64;

Query Match 18.2%; Score 48; DB 2; Length 61;
Best Local Similarity 26.5%; Pred. No. 19;
Matches 13; Conservative 7; Mismatches 19; Indels 10; Gaps 2;

OY 2 CGPCSE-----RRKHLFVDDPQTCCKSCKNMTDSRCAROLELNER 41
| | | | | | | | | | | | | | | | | | | | |
Db: 14 CGECADSCPSVLEMKGKAFVNPDDC-LGCETCVSCPSGAVTLER 61

RESULT 14
O9VE14 PRELIMINARY; PRT; 66 AA.
AC O9VE14;
DT 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DT 01-MAY-2000 (TREMBlrel. 13, Last annotation update)
DE CG7606 PROTEIN.
GN CG7606.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Eterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.

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OX NCBI_TaxID=7227;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-BERKELEY;
RX MEDLINE=20196006; PubMed=10731132;
RA Adams M.D., Celinker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galie R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sultion G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers J.-H.C., Blazek R.G., Champe M., Pfeiffer B.D.,
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Milos G.L.G.,
RA Abril J.F., Abghayani A., An H.-J., Andrews-Frankoch C., Baldwin D.,
RA Baller R.W., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Borokova D., Botchan M.R., Bouck J., Brokstein P., Brotlier P.,
RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferrera S., Fleischmann W.,
RA Posler C., Gabriellian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D., Helman T.J., Hernandez J.R., Honck J.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Idegum C.,
RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kuip D., Lai Z.,
RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Paclet J.M.,
RA Palazzolo M., Pittman G.S., Pan S., Plessner D., Puri V., Reese M.G.,
RA Reinert K., Remington K., Saunders R.D.C., Scheefer F., Shen H.,
RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Svirskas R., Teector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissbach J.,
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA Zhang X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RT "The genome sequence of Drosophila melanogaster.";
RL Science 287:2185-2195(2000).
DR EMBL; AE003718; AAP5437.1;
DR FlyBase; FBgn0040565; CG7606.
SQ SEQUENCE 66 AA; 6812 MW; 8151AF9D3BFB5FC CRC64;

Query Match 18.2%; Score 48; DB 5; Length 66;
Best Local Similarity 28.1%; Pred. No. 21;
Matches 9; Conservative 6; Mismatches 13; Indels 4; Gaps 1;

OY 14 VDDPQTCCKSCKNMTDSRCAROLELNERTCRC 45
| | | | | | | | | | | | | | | | | | | | |
Db: 22 VEEPEOVECGCGCGPC---ISCGSRSCGC 49

RESULT 15
O82789 PRELIMINARY; PRT; 81 AA.
AC O82789;
DT 01-NOV-1998 (TREMBlrel. 08, Created)
DT 01-NOV-1998 (TREMBlrel. 08, Last sequence update)
DT 01-NOV-1998 (TREMBlrel. 08, Last annotation update)
DE POLLEN COAT PROTEIN CLASS 'A', NO. 1 PRECURSOR (FRAGMENT).
GN PCP-A1.
OS Brassica oleracea (Cauliflower).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids II; Brassicales; Brassicaceae; Brassica.
OX NCBI_TaxID=3712;
RN [1]
RP SEQUENCE FROM N.A.

```


GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: January 31, 2002, 11:20:39 ; Search time 10.04 Seconds

(without alignments)
164.334 Million cell updates/sec

Title: US-09-579-420-1

Perfect score: 264
Sequence: 1 PCGPCSERKHLFVDPQTC.....NTDSRCKAROLELNERTCRC 45

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 100059 seqs, 36664827 residues

Total number of hits satisfying chosen parameters: 11805

Minimum DB seq length: 0

Maximum DB seq length: 100

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_39:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the distribution, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	58	22.0	83	1	IM10_ARATH
2	54	20.5	73	1	MT_DREPO
3	54	20.5	74	1	MT1_CABEL
4	53.5	20.3	62	1	MT2_CABEL
5	53	20.1	62	1	MT_XENLA
6	53	20.1	63	1	MT_CHICK
7	53	20.1	66	1	MT3_RAT
8	53	20.1	68	1	MT3_MOUSE
9	52.5	19.9	68	1	CRS5_YEAST
10	52	19.7	63	1	MT2_COLLI
11	52	19.7	68	1	MT3_HUMAN
12	51.5	19.5	58	1	MT1_SCYSE
13	51.5	19.5	67	1	IBB1_DIOGL
14	51	19.3	68	1	MT3_BOVIN
15	51	19.3	68	1	MT3_HORSE
16	51	19.3	68	1	MT3_PIG
17	51	19.3	74	1	MT_CRAVI
18	51	19.3	91	1	ACCD_ANTFO
19	49.5	18.8	59	1	MT1_CAUST
20	49	18.6	35	1	SCXP_ANDMA
21	49	18.6	96	1	HMVA_MERJA
22	48.5	18.4	58	1	MT_POTPO
23	48.5	18.4	87	1	OM3_CHIPS
24	48	18.2	58	1	MT2_CASTI
25	47.5	18.0	62	1	MT4_HUMAN
26	47.5	18.0	71	1	MT21_MYTED
27	47.5	18.0	82	1	IBB1_PHANAN
28	47	17.8	57	1	MT2_SCYSE
29	47	17.8	60	1	MTA_THERC
30	46.5	17.6	58	1	MT_ASTERL
31	46	17.4	51	1	MT2_CANCA
32	46	17.4	58	1	MT_CARMA
33	46	17.4	60	1	MT_CYPCA

34	46	17.4	72	1	MT11_MYTED	P80246 mytilus edu
35	46	17.4	85	1	EC2_ARATH	Q42377 arabidopsis
36	45.5	17.2	36	1	SCK3_LEIOH	P45660 leirurus qui
37	45.5	17.2	58	1	MT1_HOMAM	P29499 homarus ame
38	45.5	17.2	60	1	MT_AMBME	Q42152 ambystoma m
39	45.5	17.2	61	1	MT_C_YEAST	P07215 saccharomyc
40	45.5	17.2	92	1	NEU2_HORSE	P01182 equus cabal
41	44.5	16.9	62	1	MT4_MOUSE	P47945 mus musculu
42	44.5	16.9	63	1	IBB_VICPA	P24661 vicia faba
43	44.5	16.9	91	1	HRK_HUMAN	P00198 homo sapien
44	44	16.7	49	1	HSP1_PTC	P04101 sus scrofa
45	44	16.7	64	1	MTCO_HELPO	P55947 helix pomat

ALIGNMENTS

RESULT	1	IM10_ARATH	STANDARD;	PRT;	83 AA.
AC	Q9ZM33;				
DT	20-AUG-2001 (Rel. 40, Last sequence update)				
DT	20-AUG-2001 (Rel. 40, Last sequence update)				
DE	MITOCHONDRIAL IMPORT INNER MEMBRANE TRANSLOCASE SUBUNIT TIM10.				
GN	TIM10 OR AT2G29530 OR F16P2.9.				
OS	Arabidopsis thaliana (Mouse-ear cress).				
OC	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;				
OC	Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;				
OC	eurosid II; Brassicales; Brassicaceae; Arabidopsis.				
OX	NCBI_TaxID=3702;				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RA	Bauer M.F., Brunner M., Hofmann S.;				
RT	"Cloning and mapping of the Tim10/DDP gene family encoding small zinc				
RT	finger proteins involved in mitochondrial carrier import."				
RL	Submitted (MAY-1999) to the EMBL/GenBank/DBJ databases.				
RN	[2]				
RP	SEQUENCE FROM N.A.				
RC	SPRAIN-CV. COLUMBIA;				
RX	MEDLINE=20083487; PubMed=10617197;				
RA	Lin X., Kaul S., Rounsley S.D., Shea T.P., Benito M.-I., Town C.D.,				
RA	Fujii C.Y., Mason T.M., Bowman C.L., Barnstead M.E., Feldblum T.V.,				
RA	Buell C.R., Ketchum K.A., Lee J.J., Ronning C.M., Koo H.L.,				
RA	Moffat K.S., Cronin L.A., Shen M., Vanden S.E., Umayam L.,				
RA	Talton L.J., Gill J.E., Adams M.D., Carrera A.J., Creasy T.H.,				
RA	Goodman H.M., Somerville C.R., Copenhagen G.P., Preuss D.,				
RA	Nierman W.C., White O., Eisen J.A., Salzberg S.L., Fraser C.M.,				
RT	Venter J.C.;				
RT	"Sequence and analysis of chromosome 2 of the plant Arabidopsis				
RL	thaliana."				
CC	Nature 402:761-768(1999).				
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration				
CC	between the Swiss Institute of Bioinformatics and the EMBL Outstation -				
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CC	use by non-profit institutions as long as its content is in no way				
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CC	entities requires a license agreement (See http://www.isb-sib.ch/announce/				
CC	or send an email to license@isb-sib.ch).				
DR	EMBL: AF150093; AAD39999.1; -				
DR	EMBL: AC004561; AAC95186.1; -				
KW	Transport; Protein transport; Translocation; Mitochondrion;				
KW	Inner membrane.				
SO	SEQUENCE 83 AA: 9339 MW: 135519B3FEEF331 CRC64:				

Query Match 22.0%; Score 58; DB 1; Length 83;
Best Local Similarity 39.0%; Pred. No. 1.6; Indels 4; Gaps 2;
Matches 16; Conservative 4; Mismatches 17;
7 ERRKHLFVDPQTCCKNTDSRCKAROLELNERTC--RC 45

Db 23 EYRVEIFNKLAOTCFNKCC--VDKRYKEAEELMNGENSCIDRC 61

RESULT 2

MT_DREPO STANDARD: PRT: 73 AA.

AC 094550;

DT 01-NOV-1997 (Rel. 35, Created)

DT 01-NOV-1997 (Rel. 35, Last sequence update)

DT 01-NOV-1997 (Rel. 35, Last annotation update)

DE METALLOTHIONEIN.

OS Dreissena polymorpha (Zebra mussel).

OC Eukaryota; Metazoa; Mollusca; Bivalvia; Heterococoncha; Veneroida;

OC Dreissenoida; Dreissenidae; Dreissena.

NCBI_TaxId=45954;

ON 11

RP SEQUENCE FROM N.A.

RA Sezekan S.R., Engelken J., Hildebrandt A.;

RL Submitted (SEP-1996) to the EMBL/GenBank/DBJ databases.

RN [2]

RP SEQUENCE OF 2-40.

RA Sezekan S.R., Engelken J., Hildebrandt A.;

RL Submitted (JUL-1997) to the SWISS-PROT data bank.

CC -1- FUNCTION: THE METALLOTHIONEINS ARE INVOLVED IN THE CELLULAR

CC SEQUESTRATION OF TOXIC METAL IONS (BY SIMILARITY).

CC -1- SIMILARITY: BELONGS TO FAMILY 2 IN METALLOTHIONEIN SUPERFAMILY.

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CC

DR EMBL; U67347; AAB07548.1; -

DR HSSP; P02795; 2MHU.

DR InterPro: IPR001008; Metallthion_mollusc.

DR PRINTS; PR00875; MTMOLLUSC.

KW Metal-binding; Metal-thiolate cluster; Chelation; Cadmium.

SQ SEQUENCE 73 AA; 7364 MW; DD3398705C4DAEE9 CRC64;

Query Match 20.5%; Score 54; DB 1; Length 73;

Best Local Similarity 31.1%; Pred. No. 4.3; 11; Indels 16; Gaps 3;

Matches 14; Conservative 4; Mismatches 11; Indels 16; Gaps 3;

OY 3 GPCSERRKHLFVDPQTKC--SCKNTDSRCAROLELNERTCRC 45

Db 18 GSCS-----DCSNCKGSGDCKSKPCNCGKNV-----TCKC 48

RESULT 3

MT1_CAEEL

ID MT1_CAEEL STANDARD: PRT: 74 AA.

AC P17511;

DT 01-AUG-1990 (Rel. 15, Created)

DT 01-AUG-1990 (Rel. 15, Last sequence update)

DT 20-AUG-2001 (Rel. 40, Last annotation update)

DE METALLOTHIONEIN-1 (MT-1).

MTL-1 OR MET-1 OR K1169.6.

GN Caenorhabditis elegans.

OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;

OC Rhabditidae; Peloderinae; Caenorhabditis.

NCBI_TaxId=6239;

ON 11

RP SEQUENCE FROM N.A.

RA Slice L.W., Freedman J.H., Rubin C.S.;

RT "Purification, characterization, and cDNA cloning of a novel

RT metallochionein-like, cadmium-binding protein from Caenorhabditis

RT elegans.";

RL J. Biol. Chem. 265:256-263(1990).

RN [2]

RP SEQUENCE FROM N.A., AND SEQUENCE OF 1-24.

RC STRAIN-BRISTOL N2;

RX MEDLINE=90262552; PubMed=2344361;

RA Imagawa M., Onozawa T., Okumura K., Osada S., Nishihara T., Kondo M.;

RT "Characterization of metallothionein cDNAs induced by cadmium in the

RT nematode Caenorhabditis elegans.";

RL Biochem. J. 268:237-240(1990).

RN [3]

RP SEQUENCE FROM N.A.

RX MEDLINE=9315063; PubMed=8428932;

RA Freedman J.H., Slice L.W., Dixon D., Fire A., Rubin C.S.;

RT "The novel metallothionein genes of Caenorhabditis elegans.

RT structural organization and inducible, cell-specific expression.";

RL J. Biol. Chem. 268:2554-2564(1993).

RN [4]

RP SEQUENCE FROM N.A.

RC STRAIN-BRISTOL N2;

RX MEDLINE=95151184; PubMed=7848551;

RA Kugawa F., Yamamoto H., Osada S., Aoki M., Imagawa M., Nishihara T.;

RT metal inducibility in mammalian culture cells.";

RL Biomed. Environ. Sci. 7:222-231(1994).

RN [5]

RP SEQUENCE FROM N.A.

RA Greco T., Bradshaw H.;

RL Submitted (JUL-1996) to the EMBL/GenBank/DBJ databases.

CC -1- FUNCTION: THIS PROTEIN BINDS CATIONS OF SEVERAL TRANSITION

CC ELEMENTS.

CC -1- INDUCTION: BY CADMIUM.

CC ARE THOUGHT TO BE THE METAL-BINDING SITES IN OTHER

CC METALLOTHIONEINS.

CC -1- SIMILARITY: BELONGS TO FAMILY 6 IN METALLOTHIONEIN SUPERFAMILY.

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CC

DR EMBL; M92909; AAA28110.1; -

DR EMBL; X53244; CAA37334.1; -

DR EMBL; D17364; BAA04180.1; -

DR EMBL; U64853; AAB04979.1; -

DR PIR; S09714; S09714.

DR PIR; B45206; B45206.

DR HSSP; P04355; 4MT2.

DR WormPep; K1169.6; CE07379.

DR InterPro: IPR000853; Metallthion_nemat.

DR PRINTS; PR00876; MTNEMATODE.

KW Metal-binding; Metal-thiolate cluster; Chelation; Cadmium.

FT INIT MET 0

FT CONFLICT 22 22 D -> G (IN REF. 2; AA SEQUENCE).

SQ SEQUENCE 74 AA; 7959 MW; DA0D00C9FD6240C3 CRC64;

Query Match 20.5%; Score 54; DB 1; Length 74;

Best Local Similarity 34.6%; Pred. No. 4.4; 7; Indels 8; Gaps 1;

Matches 9; Conservative 2; Mismatches 7; Indels 8; Gaps 1;

OY 20 CKSCCKNTDSRCAROLELNERTCRC 45

Db 2 CKSCCKNKCKCKGDK-----CEC 19

RESULT 4

MT2_CAEEL

ID WT2.CAEEL STANDARD: PRT: 62 AA.
 AC p17512;
 DT 01-AUG-1990 (Rel. 15, Created)
 DT 01-AUG-1990 (Rel. 15, Last sequence update)
 DT 20-AUG-2001 (Rel. 40, Last annotation update)
 DE METALLOTHIONEIN-II (MT-II) (METALLOTHIONEIN-LIKE PROTEIN) (MT-CE).
 GN MT-2 OR MET-2 OR T0865.10.
 OS Caenorhabditis elegans.
 OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditidae;
 OC Rhabditidae; Pelodierinae; Caenorhabditis.
 OX NCBI_TaxID=6239;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=90094407; PubMed=2294106;
 RA Slice L.W., Freedman J.H., Rubin C.S.;
 RT "Purification, characterization, and cDNA cloning of a novel
 RT metallothionein-like, cadmium-binding protein from Caenorhabditis
 RT elegans.";
 RL J. Biol. Chem. 265:256-263(1990).
 RN [2]
 RP SEQUENCE FROM N.A., AND SEQUENCE OF 1-14.
 RC STRAIN-BRISTOL N2;
 RX MEDLINE=90262552; PubMed=2344361;
 RA Imagawa M., Onozawa T., Okumura K., Osada S., Nishihara T., Kondo M.;
 RT "Characterization of metallothionein cDNAs induced by cadmium in the
 RT nematode Caenorhabditis elegans.";
 RL Biochem. J. 268:237-240(1990).
 RN [3]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=93155063; PubMed=8428932;
 RA Freedman J.H., Slice L.W., Dixon D., Fire A., Rubin C.S.;
 RT "The novel metallothionein genes of Caenorhabditis elegans.
 RT Structural organization and inducible, cell-specific expression.";
 RL J. Biol. Chem. 268:2554-2564(1993).
 RN [4]
 RP SEQUENCE FROM N.A.
 RC STRAIN-BRISTOL N2;
 RX MEDLINE=95151184; PubMed=7848551;
 RA Kugawa F., Yamamoto H., Osada S., Aoki M., Imagawa M., Nishihara T.;
 RT "Metallothionein genes in the nematode Caenorhabditis elegans and
 RT metal inducibility in mammalian culture cells.";
 RL Biomed. Environ. Sci. 7:222-231(1994).
 RN [5]
 RP SEQUENCE FROM N.A.
 RC STRAIN-BRISTOL N2;
 RA Slave R.;
 RT Submitted (NOV-1996) to the EMBL/GenBank/DBJ databases.
 RL -1- FUNCTION: THIS PROTEIN BINDS CATIONS OF SEVERAL TRANSITION
 CC ELEMENTS.
 CC -1- INDUCTION: BY CADMIUM.
 CC -1- DOMAIN: ALL CYSTEINE RESIDUES ARE ARRANGED IN C-X-C GROUPS. THESE
 CC ARE THOUGHT TO BE THE METAL-BINDING SITES IN OTHER
 CC METALLOTHIONEINS.
 CC -1- SIMILARITY: BELONGS TO FAMILY 6 IN METALLOTHIONEIN SUPERFAMILY.
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 CC -----
 CC EMBL: M92910; AAA28111.1; -
 CC EMBL: M32386; AAA28117.1; -
 CC EMBL: M32387; AAA28118.1; -
 CC EMBL: X53245; CA37335.1; -
 CC EMBL: D17365; BAA04181.1; -
 CC EMBL: Z81589; CAB61028.1; -
 CC PIR: A34905; A34905.
 CC PIR: S09715; S09715.
 CC PIR: A45206; A45206.
 CC HSSP: P04355; 4MT2.

DR NormRep: T0865.10; CE25109.
 DR InterPro: IPR000853; Metlthion_nemat.
 DR PRINTS: PR00876; MTNEMATODE.
 KW Metal-binding; Metal-chiolate cluster; Chelation; Cadmium.
 FT INT MET 0 0
 SQ SEQUENCE 62 AA; 6462 MW; 5D33797A1CDBD797 CRC64;
 Query Match 20.3%; Score 53.5; DB 1; Length 62;
 Best Local Similarity 34.6%; Pred. No. 4.3;
 Matches 9; Conservative 2; Mismatches 10; Indels 5; Gaps 1;
 Oy 20 CKCCKMTDSCRKARQLEINERTCRC 45
 Db 2 CKCCKNQCNCNT-----GTRKDCD 22
 RESULT 5
 MT_XENIA STANDARD: PRT: 62 AA.
 ID MT_XENIA
 AC 005890;
 DT 01-FEB-1994 (Rel. 28, Created)
 DT 01-FEB-1994 (Rel. 28, Last sequence update)
 DT 01-NOV-1997 (Rel. 35, Last annotation update)
 DE METALLOTHIONEIN.
 GN MT-A.
 OS Xenopus laevis (African clawed frog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipridae; Pipidae;
 OC Xenopodinae; Xenopus.
 OX NCBI_TaxID=8335;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Liver;
 RX MEDLINE=93263990; PubMed=8494609;
 RA St Jacques E., Seguin C.;
 RT "Cloning and nucleotide sequence of a complementary DNA encoding
 RT Xenopus laevis metallothionein: mRNA accumulation in response to
 RT heavy metals.";
 RL DNA Cell Biol. 12:329-340(1993).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=93263991; PubMed=8494610;
 RA Muller J.-P., Wouters-Tyrou D., Errais N.-E., Vedel M., Touzet N.,
 RA Mesnard J., Sautiere P., Wegnez M.;
 RT "Molecular cloning and expression of a metallothionein mRNA in
 RT Xenopus laevis.";
 RL DNA Cell Biol. 12:341-349(1993).
 CC -1- FUNCTION: METALLOTHIONEINS HAVE A HIGH CONTENT OF CYSTEINE
 CC RESIDUES THAT BIND VARIOUS HEAVY METALS.
 CC -1- DOMAIN: CLASS I METALLOTHIONEINS CONTAIN 2 METAL-BINDING DOMAINS:
 CC FOUR DIVALENT IONS ARE CHELATED WITHIN CLUSTER A OF THE ALPHA
 CC DOMAIN AND ARE COORDINATED VIA CYSTEINYL THIOLATE BRIDGES TO 11
 CC CYSTEINE LIGANDS. CLUSTER B, THE CORRESPONDING REGION WITHIN THE
 CC BETA DOMAIN, CAN LIGATE THREE DIVALENT IONS TO 9 CYSTEINES.
 CC -1- SIMILARITY: BELONGS TO FAMILY 1 IN METALLOTHIONEIN SUPERFAMILY.
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 CC -----
 CC EMBL: U14649; AAB60616.1; -
 CC EMBL: M96729; AAB5949.1; -
 CC EMBL: X69380; CAA49177.1; -
 CC HSSP: P04355; 1MRT.
 CC InterPro: IPR003019; Metallothion.
 CC InterPro: IPR000066; Metlthion_vert.
 CC Pfam: PF00131; metalthio.1.
 CC PRINTS: PR00860; MTVERTEBRATE.

DR PROSITE: PS00203; METALLOTHIONEIN_VRT; 1.
 KW Metal-binding; Metal-Chiolate cluster; Chelation; Acetylation.
 FT MOD_RES 1 1 ACETYLATION.
 FT DOMAIN 1 1 30 ALPHA.
 FT METAL 31 62 BETA.
 FT METAL 6 6 CLUSTER B.
 FT METAL 8 8 CLUSTER B.
 FT METAL 14 14 CLUSTER B.
 FT METAL 16 16 CLUSTER B.
 FT METAL 20 20 CLUSTER B.
 FT METAL 22 22 CLUSTER B.
 FT METAL 25 25 CLUSTER B.
 FT METAL 27 27 CLUSTER B.
 FT METAL 30 30 CLUSTER B.
 FT METAL 34 34 CLUSTER A.
 FT METAL 35 35 CLUSTER A.
 FT METAL 37 37 CLUSTER A.
 FT METAL 38 38 CLUSTER A.
 FT METAL 42 42 CLUSTER A.
 FT METAL 45 45 CLUSTER A.
 FT METAL 49 49 CLUSTER A.
 FT METAL 51 51 CLUSTER A.
 FT METAL 58 58 CLUSTER A.
 FT METAL 60 60 CLUSTER A.
 FT METAL 61 61 CLUSTER A.
 SQ SEQUENCE 62 AA; 6403 MW; AF7329487A3C7982 CRC64;

Query Match 20.18; Score 53; DB 1; Length 62;
 Best Local Similarity 33.38; Pred. No. 4.9;
 Matches 12; Conservative 2; Mismatches 16; Gaps 1;

QY 16 DPORCK-----CCKNTDNRKAROLELNRTCRC 45
 Db 2 DPQCKCETGASCSCGTTCCSNCKTCKKSCCSC 37

RESULT 6
 MT_CHICK
 ID MT_CHICK STANDARD; PRT; 63 AA.
 AC P09576:
 DT 01-MAR-1989 (Rel. 10, Created)
 DT 01-MAR-1989 (Rel. 10, Last sequence update)
 DT 15-DEC-1998 (Rel. 37, Last annotation update)
 DE METALLOTHIONEIN (MT).
 OS Gallus gallus (Chicken), *Melagris gallopavo* (Common turkey),
 OS *Phasianus colchicus colchicus* (Ring-necked pheasant),
 OS *Anas platyrhynchos* (Domestic duck), and
 OS *Cairina moschata* (Muscovy duck).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
 OC Gallus.
 OX NCBI_TaxID=9031, 9103, 9057, 8839, 8855;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC SPECIES=Chicken; STRAIN=WHITE LEGHORN;
 RX MEDLINE=88124253; PubMed=3340548;
 RA Wei D., Andrews G.K.;
 RT "Molecular cloning of chicken metallothionein. Deduction of the
 RT complete amino acid sequence and analysis of expression using cloned
 RT cDNA.";
 RL Nucleic Acids Res. 16:537-553(1988).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC SPECIES=Chicken;
 RX MEDLINE=90034180; PubMed=2806910;
 RA Fernando L.P., Andrews G.K.;
 RT "Cloning and expression of an avian metallothionein-encoding gene.";
 RL Gene 81:177-183(1989).
 RN [3]
 RP SEQUENCE.
 RC SPECIES=Chicken; TISSUE=Liver;
 RX MEDLINE=88124831; PubMed=2448773;

RA McCormick C.C., Fullmer C.S., Garvey J.S.;
 RT "Amino acid sequence and comparative antigenicity of chicken
 RT metallothionein.";
 RL Proc. Natl. Acad. Sci. U.S.A. 85:309-313(1988).
 RN [4]
 RP SEQUENCE.
 RC SPECIES=Chicken;
 RX MEDLINE=89141100; PubMed=2645390;
 RA Fernando L.P., Wei D., Andrews G.K.;
 RT "Structure and expression of chicken metallothionein.";
 RL J. Nutr. 119:309-318(1989).
 RN [5]
 RP SEQUENCE FROM N.A.
 RC SPECIES=A.platyrhynchos, and C.moschata; TISSUE=Liver;
 RA Lin L.-Y., Lee Y.J.;
 RL Submitted (SEP-1995) to the EMBL/GenBank/DBJ databases.
 RN [6]
 RP SEQUENCE.
 RC SPECIES=A.platyrhynchos, and C.moschata;
 RX MEDLINE=90226357; PubMed=2327997;
 RA Lin L.-Y., Huang P.C.;
 RT "Complete homology in metallothionein from two genera of ducks and
 RT their hybrids.";
 RL Biochem. Biophys. Res. Commun. 168:182-187(1990).
 RN [7]
 RP SEQUENCE.
 RC SPECIES=Mule duck [Common duck X Muscovy duck];
 RX MEDLINE=91027866; PubMed=2223844;
 RA Lin L.-Y., Liu L.-F., Tam M.F., Huang P.C., Vestling M., Fenselau C.;
 RT "Primary sequence of duck metallothionein.";
 RL Biochim. Biophys. Acta 1041:31-35(1990).
 RN [8]
 RP SEQUENCE OF 15-57 FROM N.A.
 RC SPECIES=M.gallopavo, and P.colchicus; TISSUE=Liver;
 RX MEDLINE=93247065; PubMed=8483164;
 RA Shartzer K.L., Kage K., Sobieski R.J., Andrews G.K.;
 RT "Evolution of avian metallothionein: DNA sequence analyses of the
 RT turkey metallothionein gene and metallothionein cDNAs from pheasant
 RT and quail.";
 RL J. Mol. Evol. 36:255-262(1993).
 CC -1- FUNCTION: METALLOTHIONEINS HAVE A HIGH CONTENT OF CYSTEINE
 CC RESIDUES THAT BIND VARIOUS HEAVY METALS.
 CC -1- DOMAIN: CLASS I METALLOTHIONEINS CONTAIN 2 METAL-BINDING DOMAINS:
 CC FOUR DIVALENT IONS ARE CHELATED WITHIN CLUSTER A OF THE ALPHA
 CC DOMAIN AND ARE COORDINATED VIA CYSTEINYL THIOLATE BRIDGES TO 11
 CC CYSTEINE LIGANDS. CLUSTER B, THE CORRESPONDING REGION WITHIN THE
 CC BETA DOMAIN, CAN LIGATE THREE DIVALENT IONS TO 9 CYSTEINES.
 CC -1- SIMILARITY: BELONGS TO FAMILY 1 IN METALLOTHIONEIN SUPERFAMILY.
 CC -----
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 CC or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL: X06749; CAA29924.1; -;
 DR EMBL: X62514; CAA44372.1; -;
 DR EMBL: X62510; CAA44369.1; -;
 DR EMBL: U34231; AAC60048.1; -;
 DR EMBL: U34230; AAC60047.1; -;
 DR PIR: A28113; A28113.
 DR PIR: J00030; J00030.
 DR PIR: S01750; S01750.
 DR PIR: S13154; S13154.
 DR PIR: A34620; A34620.
 DR PIR: A34958; A34958.
 DR PIR: B34620; B34620.
 DR PIR: C34620; C34620.
 DR PIR: S18180; S18180.
 DR PIR: S18182; S18182.
 DR PIR: S33381; S33381.

DR HSSP: P02795; 2MHU.
 DR InterPro: IPR003019; Metallthion.
 DR InterPro: IPR000006; Metallthion_vert.
 DR Pfam: PF00131; metalthio; 1.
 DR PRINTS: PR00860; MTEVERTERATE.
 DR PROSITE: PS00203; METALLOTHIONEIN_VRT; 1.
 KW Metal-binding; Metal-thiolate cluster; Chelation; Zinc.
 FT DOMAIN 1 30
 FT METAL 31 63 ALPHA.
 FT METAL 6 6 CLUSTER B.
 FT METAL 8 8 CLUSTER B.
 FT METAL 14 14 CLUSTER B.
 FT METAL 16 16 CLUSTER B.
 FT METAL 20 20 CLUSTER B.
 FT METAL 22 22 CLUSTER B.
 FT METAL 25 25 CLUSTER B.
 FT METAL 27 27 CLUSTER B.
 FT METAL 30 30 CLUSTER B.
 FT METAL 34 34 CLUSTER A.
 FT METAL 35 35 CLUSTER A.
 FT METAL 37 37 CLUSTER A.
 FT METAL 38 38 CLUSTER A.
 FT METAL 42 42 CLUSTER A.
 FT METAL 45 45 CLUSTER A.
 FT METAL 49 49 CLUSTER A.
 FT METAL 51 51 CLUSTER A.
 FT METAL 59 59 CLUSTER A.
 FT METAL 61 61 CLUSTER A.
 FT METAL 62 62 CLUSTER A.
 SO SEQUENCE 63 AA; 6461 MW; 0062422501B9CC84 CRC64;

Query Match 20.1%; Score 53; DB 1; Length 63;
 Best Local Similarity 30.0%; Pred. No. 4.9;
 Matches 12; Conservative 4; Mismatches 10; Indels 14; Gaps 2;

OY 16 DPOTCKC-----SKNDSRCKAROLEINERTCRC 45
 DB 2 DPQDCTCAAGDSCSCAGSCCKNCRCRS----CRKSCCSC 37

RESULT 7
 ID MT3_RAT STANDARD; PRT; 66 AA.
 AC P37361;
 DT 01-OCT-1994 (Rel. 30, Created)
 DT 01-OCT-1994 (Rel. 30, Last sequence update)
 DT 15-JUL-1998 (Rel. 36, Last annotation update)
 DE METALLOTHIONEIN-III (MT-III) (GROWTH INHIBITORY FACTOR) (GIF).
 GN MT3.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_TaxID=10116;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA MEDLINE=94018480; PubMed=8412560;
 RA Kobayashi H., Uchida Y., Ihara Y., Nakajima K., Kohsaka S.,
 RA Miyake T., Tsuji S.;
 RA "Molecular cloning of rat growth inhibitory factor cDNA and the
 RA expression in the central nervous system."
 RA Brain Res. Mol. Brain Res. 19:188-194(1993).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Glial tumor;
 RA Amoureux M.C., Rehsaus E., Murch T., Colpaert F.C., Pauwels P.J.;
 RA Submitted (JUL-1995) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN=SPRAGUE-DAWLEY;
 RA Chapman G.A., Kille P.;
 RA Submitted (SEP-1996) to the EMBL/GenBank/DBJ databases.
 CC -1- FUNCTION: BINDS HEAVY METALS. CONTAINS ZINC AND COPPER ATOMS AND

CC ONLY A NEGLECTIBLE AMOUNT OF CADMIUM (BY SIMILARITY).
 CC -1- TISSUE SPECIFICITY: BRAIN.
 CC -1- SIMILARITY: BELONGS TO FAMILY 1 IN METALLOTHIONEIN SUPERFAMILY.
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 CC
 CC EMBL: S65838; AAB28366.1; -
 CC EMBL: X89603; CAA61762.1; -
 CC EMBL: Y08235; CAA69404.1; -
 CC HSSP: P18055; IMRB.
 DR InterPro: IPR003019; Metallthion.
 DR InterPro: IPR000006; Metallthion_vert.
 DR Pfam: PF00131; metalthio; 1.
 DR PRINTS: PR00860; MTEVERTERATE.
 DR PROSITE: PS00203; METALLOTHIONEIN_VRT; 1.
 KW Metal-binding; Metal-thiolate cluster; Chelation; Zinc; Copper;
 KW Acetylation.
 FT MOD_RES 1 1 ACETYLATION (BY SIMILARITY).
 FT DOMAIN 1 30 BETA.
 FT METAL 31 66 ALPHA.
 FT METAL 6 6 CLUSTER B (BY SIMILARITY).
 FT METAL 8 8 CLUSTER B (BY SIMILARITY).
 FT METAL 14 14 CLUSTER B (BY SIMILARITY).
 FT METAL 16 16 CLUSTER B (BY SIMILARITY).
 FT METAL 20 20 CLUSTER B (BY SIMILARITY).
 FT METAL 22 22 CLUSTER B (BY SIMILARITY).
 FT METAL 25 25 CLUSTER B (BY SIMILARITY).
 FT METAL 27 27 CLUSTER B (BY SIMILARITY).
 FT METAL 30 30 CLUSTER B (BY SIMILARITY).
 FT METAL 34 34 CLUSTER A (BY SIMILARITY).
 FT METAL 35 35 CLUSTER A (BY SIMILARITY).
 FT METAL 37 37 CLUSTER A (BY SIMILARITY).
 FT METAL 38 38 CLUSTER A (BY SIMILARITY).
 FT METAL 42 42 CLUSTER A (BY SIMILARITY).
 FT METAL 45 45 CLUSTER A (BY SIMILARITY).
 FT METAL 49 49 CLUSTER A (BY SIMILARITY).
 FT METAL 51 51 CLUSTER A (BY SIMILARITY).
 FT METAL 62 62 CLUSTER A (BY SIMILARITY).
 FT METAL 64 64 CLUSTER A (BY SIMILARITY).
 FT METAL 65 65 CLUSTER A (BY SIMILARITY).
 SO SEQUENCE 66 AA; 6809 MW; BE7538E85664EBF8 CRC64;

Query Match 20.1%; Score 53; DB 1; Length 66;
 Best Local Similarity 35.3%; Pred. No. 5.2;
 Matches 12; Conservative 5; Mismatches 5; Indels 12; Gaps 3;

OY 16 DPOTCKC-----SKNDSRCKAROLEINERTCRC 45
 DB 2 DPQDCTCAAGDSCSCAGSCCKNCRCRS----CRKSCCSC 37

RESULT 8
 ID MT3_MOUSE STANDARD; PRT; 68 AA.
 AC P28184;
 DT 01-DEC-1992 (Rel. 24, Created)
 DT 01-DEC-1992 (Rel. 24, Last sequence update)
 DT 01-NOV-1997 (Rel. 35, Last annotation update)
 DE METALLOTHIONEIN-III (MT-III) (GROWTH INHIBITORY FACTOR) (GIF).
 GN Mus musculus (Mouse).
 OS Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.

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RC TISSUE=Brain;
RA MEDLINE=9235292; PubMed=1631128;
RX Palmer R.D., Findley S.D., Whitmore T.E., Duram D.M.;
RA "MT-III, a brain-specific member of the metallothionein gene family.";
RL Proc. Natl. Acad. Sci. U.S.A. 89:6333-6337(1992).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=94314230; PubMed=8039715;
RA Naruse S., Igarashi S., Furuya T., Kobayashi H., Miyake T.,
RA Tsuji S.;
RT "Structures of the human and mouse growth inhibitory factor-encoding
genes";
RL Gene 144:283-287(1994).
CC -1- FUNCTION: INHIBITS SURVIVAL AND NEURITE FORMATION OF CORTICAL
CC NEURONS IN VITRO.
CC -1- ONLY A NEGLIGIBLE AMOUNT OF CADMIUM (BY SIMILARITY).
CC -1- TISSUE SPECIFICITY: BRAIN.
CC -1- SIMILARITY: BELONGS TO FAMILY 1 IN METALLOTHIONEIN SUPERFAMILY.
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: M93310; AAA39529.1; -.
DR EMBL: S72046; AAB31397.1; -.
DR PIR: A46034; A46034.
DR HSP: P18055; 1MRB.
DR MGD: MGI:97173; M13.
DR InterPro: IPR003019; Metallothion.
DR InterPro: IPR000006; Metallothion_vert.
DR Pfam: PF00131; metalthio; 1.
DR PRINTS: PR00860; MTVERTBRATE.
DR PROSITE: PS00203; METALLOTHIONEIN_VRT; 1.
KW Metal-binding; Metal-chiolate cluster; Chelation; Zinc; Copper;
KW Acetylation.
FT MOD_RES 1 1 ACETYLATION (BY SIMILARITY).
FT DOMAIN 1 1 BETA.
FT DOMAIN 31 68 ALPHA.
FT METAL 6 6 CLUSTER B (BY SIMILARITY).
FT METAL 8 8 CLUSTER B (BY SIMILARITY).
FT METAL 14 14 CLUSTER B (BY SIMILARITY).
FT METAL 16 16 CLUSTER B (BY SIMILARITY).
FT METAL 20 20 CLUSTER B (BY SIMILARITY).
FT METAL 22 22 CLUSTER B (BY SIMILARITY).
FT METAL 25 25 CLUSTER B (BY SIMILARITY).
FT METAL 27 27 CLUSTER B (BY SIMILARITY).
FT METAL 30 30 CLUSTER B (BY SIMILARITY).
FT METAL 34 34 CLUSTER A (BY SIMILARITY).
FT METAL 35 35 CLUSTER A (BY SIMILARITY).
FT METAL 37 37 CLUSTER A (BY SIMILARITY).
FT METAL 38 38 CLUSTER A (BY SIMILARITY).
FT METAL 42 42 CLUSTER A (BY SIMILARITY).
FT METAL 45 45 CLUSTER A (BY SIMILARITY).
FT METAL 49 49 CLUSTER A (BY SIMILARITY).
FT METAL 51 51 CLUSTER A (BY SIMILARITY).
FT METAL 64 64 CLUSTER A (BY SIMILARITY).
FT METAL 66 66 CLUSTER A (BY SIMILARITY).
FT METAL 67 67 CLUSTER A (BY SIMILARITY).
SQ SEQUENCE 68 AA; 7009 MW; 791AF60E38FED3CA CRC64;

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Query Match 20.1%; Score 53; DB 1; Length 68;
 Best Local Similarity 35.3%; Pred. No. 5.3;
 Matches 12; Conservative 5; Mismatches 5; Indels 12; Gaps 3;

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OY 16 DPOTKC-----SCKNDSRCKARQLEINERTC 45
DB 2 DPOTCPTGSGCTCSD-KCKC-----KGCKC 27

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RESULT 9
CRS5_YEAST STANDARD; PRT; 69 AA.
ID P41902;
AC 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DE 30-MAY-2000 (Rel. 39, Last annotation update)
DE METALLOTHIONEIN-LIKE PROTEIN CRS5.
GN CRS5 OR YOR031W.
OS Saccharomyces cerevisiae (Baker's yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Saccharomyces.
OX NCBI_Taxid=4932;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=95014318; PubMed=7929222;
RA Clotita V.C., Howard W.R., Liu X.F.;
RT "CRS5 encodes a metallothionein-like protein in Saccharomyces
cerevisiae";
RL J. Biol. Chem. 269:25295-25302(1994).
RN [2]
RP SEQUENCE FROM N.A.
RX STRAIN=S288C / FY1679;
RA de Haan M., Maarse A.C., Grievell L.A.;
RL Submitted (MAY-1995) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: CRITICAL ROLE IN COPPER (SPECIFIC) HOMEOSTASIS AND
CC DETOXIFICATION. MAY PROTECT BY DIRECTLY CHELATING AND SEQUESTERING
CC COPPER IONS.
CC -1- SIMILARITY: BELONGS TO FAMILY 13 IN METALLOTHIONEIN SUPERFAMILY.
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: L29056; AAA6061.1; -.
DR EMBL: X87331; -. NOT_ANNOTATED_CDS.
DR SGD: S0005557; CRS5.
KW Metal-binding; Metal-chiolate cluster; Chelation.
SQ SEQUENCE 69 AA; 7321 MW; CEEF91203A813FF4 CRC64;

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Query Match 19.9%; Score 52.5; DB 1; Length 69;
 Best Local Similarity 31.4%; Pred. No. 6.1;
 Matches 11; Conservative 3; Mismatches 8; Indels 13; Gaps 2;

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OY 18 QTCCK-----SCKNDSRCKARQLEINERTC 45
DB 31 ECKCKDHSTGSPCKSCGCKC-----ETTCTC 59

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RESULT 10
MT2_COLL1 STANDARD; PRT; 63 AA.
ID P15787;
AC 01-APR-1990 (Rel. 14, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DE 01-NOV-1997 (Rel. 35, Last annotation update)
DE METALLOTHIONEIN-II (MT-2).
OS Columba livia (Domestic pigeon).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Columbiformes; Columbidae; Columba.
OX NCBI_Taxid=9932;
RN [1]
RP SEQUENCE.

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RC TISSUE=Liver;
RX MEDLINE=90167121; PubMed=2407296;
RA Lin L.-Y., Lin W.C., Huang P.C.;

```

RT Pigeon metallothionein consists of two species.";
RL Biochim. Biophys. Acta 1037:248-255(1990).
CC -1- FUNCTION: METALLOTHIONEINS HAVE A HIGH CONTENT OF CYSTEINE
CC RESIDUES THAT BIND VARIOUS HEAVY METALS.
CC -1- DOMAIN CLASS I METALLOTHIONEINS CONTAIN 2 METAL-BINDING DOMAINS:
CC FOUR DIVALENT IONS ARE CHELATED WITHIN CLUSTER A OF THE ALPHA
CC DOMAIN AND ARE COORDINATED VIA CYSTEINYL THIOLATE BRIDGES TO 11
CC CYSTEINE LIGANDS. CLUSTER B, THE CORRESPONDING REGION WITHIN THE
CC BETA DOMAIN, CAN LIGATE THREE DIVALENT IONS TO 9 CYSTEINES.
CC -1- SIMILARITY: BELONGS TO FAMILY 1 IN METALLOTHIONEIN SUPERFAMILY.
DR PIR: S08191; S08191.
DR HSSP: P02795; 2MHU.
DR InterPro: IPR003019; Metallothion.
DR InterPro: IPR000006; Metallothion_vert.
DR Pfam: PF00131; metalthio; 1.
DR PRINTS: PR00860; MTVERTERATE.
DR PROSITE: PS00203; METALLOTHIONEIN_VRT; 1.
KW Metal-binding; Metal-thiolate cluster; Chelation.
FT DOMAIN 1 30
FT METAL 31 63 ALPHA.
FT METAL 6 6 CLUSTER B.
FT METAL 8 8 CLUSTER B.
FT METAL 14 14 CLUSTER B.
FT METAL 16 16 CLUSTER B.
FT METAL 20 22 CLUSTER B.
FT METAL 22 22 CLUSTER B.
FT METAL 25 25 CLUSTER B.
FT METAL 27 27 CLUSTER B.
FT METAL 30 30 CLUSTER B.
FT METAL 34 34 CLUSTER A.
FT METAL 35 35 CLUSTER A.
FT METAL 37 37 CLUSTER A.
FT METAL 38 38 CLUSTER A.
FT METAL 42 42 CLUSTER A.
FT METAL 45 45 CLUSTER A.
FT METAL 49 49 CLUSTER A.
FT METAL 51 51 CLUSTER A.
FT METAL 59 59 CLUSTER A.
FT METAL 61 61 CLUSTER A.
FT METAL 62 62 CLUSTER A.
SQ SEQUENCE 63 AA; 6452 MW; A2B84227E94C365E CRC64;

Query Match 19.7%; Score 52; DB 1; Length 63;
Best Local Similarity 30.0%; Pred. No. 6.5;
Matches 12; Conservative 4; Mismatches 10; Indels 14; Gaps 2;
QY 16 DPOTC-----SKNTDSRCKAROLELNEKTCRC 45
DB 2 DPDDCTCAGDSCSCAGSCCKCKRCOS---CRKSCCSC 37

RESULT 11
MT3_HUMAN STANDARD; PRT; 68 AA.
AC P25713;
DT 01-MAY-1992 (Rel. 22, Created)
DT 01-MAY-1992 (Rel. 22, Last sequence update)
DT 01-NOV-1997 (Rel. 35, Last annotation update)
DE METALLOTHIONEIN-III (MT-III) (GROWTH INHIBITORY FACTOR) (GIF) (GIFB).
GN MT3.
OS Homo sapiens (Human).
OC Eukaryota: Metazoa: Chordata: Vertebrata: Euteleostomi:
OC Mammalia: Eutheria: Primates: Catarrhini: Hominiidae: Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RX MEDLINE=92335292; PubMed=1631128;
RA Palmiter R.D., Findley S.D., Whitmore T.E., Duram D.M.:
RT "MT-III, a brain-specific member of the metallothionein gene family.";
RL Proc. Natl. Acad. Sci. U.S.A. 89:6333-6337(1992).
RN [2]
FT METAL

RP SEQUENCE FROM N.A., AND SEQUENCE.
RC TISSUE=Brain;
RX MEDLINE=91337462; PubMed=1873033;
RA Uchida Y., Takio K., Titani K., Ihara Y., Tomonaga M.:
RT "The growth inhibitory factor that is deficient in the Alzheimer's
RT disease brain is a 68 amino acid metallothionein-like protein.";
RL Neuron 7:337-347(1991).
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE=93099858; PubMed=1464312;
RA Tsuji S., Kobayashi H., Uchida Y., Ihara Y., Miyatake T.:
RT "Molecular cloning of human growth inhibitory factor cDNA and its
RT down-regulation in Alzheimer's disease.";
RL EMO 7. 11:4843-4850(1992).
RN [4]
RP SEQUENCE FROM N.A.
RX MEDLINE=94314230; PubMed=8039715;
RA Naruse S., Igarashi S., Furuya T., Kobayashi H., Miyatake T.,
RA Tsuji S.:
RT "Structures of the human and mouse growth inhibitory factor-encoding
RT genes.";
RL Gene 144:283-287(1994).
RN [5]
RP SEQUENCE FROM N.A.
RA Amoureux M.C., Rethaus E., Wurch T., Colpaert F.C., Pauwels P.J.:
RL Submitted (JUL-1995) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: INHIBITS SURVIVAL AND NEURITE FORMATION OF CORTICAL
CC NEURONS IN VITRO.
CC -1- FUNCTION: BINDS HEAVY METALS. CONTAINS THREE ZINC AND FOUR COPPER
CC ATOMS PER POLYPEPTIDE CHAIN AND ONLY A NEGLIGIBLE AMOUNT OF
CC CADMIUM.
CC -1- TISSUE SPECIFICITY: ABUNDANT IN A SUBSET OF ASTROCYTES IN THE
CC NORMAL HUMAN BRAIN, BUT GREATLY REDUCED IN THE ALZHEIMER'S
CC DISEASE (AD) BRAIN.
CC -1- SIMILARITY: BELONGS TO FAMILY 1 IN METALLOTHIONEIN SUPERFAMILY.
CC -----
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CC -----
DR EMBL: M93311; AAA36214.1; -;
DR EMBL: D13365; -; NOT ANNOTATED_CDS.
DR EMBL: S72043; AAB31396.1; -;
DR EMBL: X89604; CAA61763.1; -;
DR PIR: S28393; S28393.
DR PIR: B46034; B46034.
DR HSSP: P18055; 1MRB.
DR MTM: 139255; -;
DR InterPro: IPR003019; Metallothion.
DR InterPro: IPR000006; Metallothion_vert.
DR Pfam: PF00131; metalthio; 1.
DR PRINTS: PR00860; MTVERTERATE.
DR PROSITE: PS00203; METALLOTHIONEIN_VRT; 1.
KW Metal-binding; Metal-thiolate cluster; Chelation; Zinc; Copper;
KW Acetylation.
FT WOD_RES 1 1
FT DOMAIN 1 30 ACETYLATION.
FT METAL 31 68 BETA.
FT METAL 6 6 ALPHA.
FT METAL 8 8 CLUSTER B (BY SIMILARITY).
FT METAL 14 14 CLUSTER B (BY SIMILARITY).
FT METAL 16 16 CLUSTER B (BY SIMILARITY).
FT METAL 20 20 CLUSTER B (BY SIMILARITY).
FT METAL 22 22 CLUSTER B (BY SIMILARITY).
FT METAL 25 25 CLUSTER B (BY SIMILARITY).
FT METAL 27 27 CLUSTER B (BY SIMILARITY).
FT METAL 30 30 CLUSTER B (BY SIMILARITY).
FT METAL 34 34 CLUSTER A (BY SIMILARITY).
FT METAL 35 35 CLUSTER A (BY SIMILARITY).

FT METAL 37 37 CLUSTER A (BY SIMILARITY).
 FT METAL 38 38 CLUSTER A (BY SIMILARITY).
 FT METAL 42 42 CLUSTER A (BY SIMILARITY).
 FT METAL 45 45 CLUSTER A (BY SIMILARITY).
 FT METAL 49 49 CLUSTER A (BY SIMILARITY).
 FT METAL 51 51 CLUSTER A (BY SIMILARITY).
 FT METAL 64 64 CLUSTER A (BY SIMILARITY).
 FT METAL 66 66 CLUSTER A (BY SIMILARITY).
 FT METAL 67 67 CLUSTER A (BY SIMILARITY).
 SQ SEQUENCE 68 AA; 6927 MW; 59801ECF5BC8A406 CRC64;

Query Match 19.7%; Score 52; DB 1; Length 68;
 Best Local Similarity 38.2%; Pred. No. 6.9;
 Matches 13; Conservative 2; Mismatches 7; Indels 12; Gaps 3;

QY 16 DPQCKC-----SKNTSRCKARQLEINERTC 45
 DB 2 DPETCPGSGSGCTCADS-CRC-----EQCKC 27

RESULT 12
 MTL_SCYSE STANDARD; PRT; 58 AA.
 ID MTL_SCYSE
 AC P02805;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 01-NOV-1997 (Rel. 35, Last annotation update)
 DE METALLOTHIONEIN-I (MT-I).
 OS Scylla serrata (Mud crab).
 OC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;
 OC Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Brachyura;
 OC Eubrachyura; Portunoidae; Portunidae; Scylla.
 OX NCBI_Taxid=6761;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=62142340; PubMed=7061431;
 RA Lerch K., Ammer D., Olafson R.W.;
 RT "Crab metallothionein. Primary structures of metallothioneins 1 and 2."
 RT J. Biol. Chem. 257:2420-2426(1982).
 CC -1- FUNCTION: METALLOTHIONEINS HAVE A HIGH CONTENT OF CYSTEINE
 CC RESIDUES THAT BIND VARIOUS HEAVY METALS. CLASS I MTS IN MARINE
 CC CRUSTACEA ARE INVOLVED IN THE SEQUESTRATION OF ELEVATED LEVELS
 CC OF HEAVY-METAL IONS.
 CC -1- SIMILARITY: BELONGS TO FAMILY 3 IN METALLOTHIONEIN SUPERFAMILY.
 CC PIR: A03283; SMKDIS.
 DR HSSP: P55949; IDMP.
 DR InterPro: IPR003019; Metallothion.
 DR InterPro: IPR002045; Metallothion_crust.
 DR Pfam: PF00131; metalthio; 1.
 DR PRINTS: PR00858; MTCRUSTACEAN.
 KM Metal-binding; Metal-chelate cluster; Chelation.
 FT DOMAIN 1 28 BETA.
 FT METAL 29 58 ALPHA.
 FT METAL 4 4 CLUSTER B.
 FT METAL 5 5 CLUSTER B.
 FT METAL 9 9 CLUSTER B.
 FT METAL 11 11 CLUSTER B.
 FT METAL 16 16 CLUSTER B.
 FT METAL 20 20 CLUSTER B.
 FT METAL 22 22 CLUSTER B.
 FT METAL 25 25 CLUSTER B.
 FT METAL 27 27 CLUSTER B.
 FT METAL 30 30 CLUSTER B.
 FT METAL 33 33 CLUSTER A.
 FT METAL 37 37 CLUSTER A.
 FT METAL 39 39 CLUSTER A.
 FT METAL 45 45 CLUSTER A.
 FT METAL 49 49 CLUSTER A.
 FT METAL 53 53 CLUSTER A.
 FT METAL 55 55 CLUSTER A.
 FT METAL 56 56 CLUSTER A.

SQ SEQUENCE 58 AA; 6001 MW; CE8A24C590B027B8 CRC64;

Query Match 19.5%; Score 51.5; DB 1; Length 58;
 Best Local Similarity 38.5%; Pred. No. 6.9;
 Matches 10; Conservative 4; Mismatches 11; Indels 1; Gaps 1;

QY 19 TCKCS-CKNTDSRCKARQLEINERTC 43
 DB 24 SCRCSPCKSGSGCKANKEGCKTC 49

RESULT 13
 IB1_DIOGL STANDARD; PRT; 67 AA.
 ID IB1_DIOGL
 AC P82469;
 DT 30-MAY-2000 (Rel. 39, Created)
 DT 30-MAY-2000 (Rel. 39, Last sequence update)
 DT 20-AUG-2001 (Rel. 40, Last annotation update)
 DE BOWMAN-BIRK TYPE PROTEINASE INHIBITOR I (DGTI).
 OS Dioclea glabra.
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
 OC eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae; Dioclea.
 OX NCBI_Taxid=124593;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Seed;
 RX MEDLINE=99373165; PubMed=10441512;
 RA Bueno N.R., Filtz H., Auerwald E.A., Mentele R., Sampaio M.U.,
 RA Sampaio C.A.M., Oliva M.L.V.;
 RT "Primary structure of Dioclea glabra trypsin inhibitor, DGTI, a Bowman-Birk inhibitor."
 RT Biochem. Biophys. Res. Commun. 261:838-843(1999).
 RT Biochem. Biophys. Res. Commun. 261:838-843(1999).
 CC -1- FUNCTION: INHIBITS TRYPSIN BUT NOT CHYMOTRYPSIN. THE INHIBITOR
 CC CONSISTS OF 2 DOMAINS AND HAS 2 SITES OF INTERACTION WITH TRYPSIN.
 CC -1- SUBUNIT: MONOMER. ALTHOUGH DIMERIZATION MAY OCCUR IN SOLUTION.
 CC -1- TISSUE SPECIFICITY: SEED.
 CC -1- SIMILARITY: BELONGS TO THE BOWMAN-BIRK SERINE PROTEASE INHIBITORS
 CC FAMILY.

DR InterPro: IPR000877; Bowman-Birk_leg.
 DR Pfam: PF00228; Bowman-Birk_leg; 1.
 DR ProDom: PD002168; Bowman-Birk_leg; 1.
 DR SMART: SM00269; BOWB; 1.
 DR PROSITE: PS00281; BOWMAN BIRK; 1.
 KM Serine protease inhibitor.
 FT ACT_SITE 13 13 INTERACTION WITH TRYPSIN.
 FT ACT_SITE 40 40 INTERACTION WITH TRYPSIN.
 FT DISULFID 5 59 BY SIMILARITY.
 FT DISULFID 6 21 BY SIMILARITY.
 FT DISULFID 9 55 BY SIMILARITY.
 FT DISULFID 11 19 BY SIMILARITY.
 FT DISULFID 29 36 BY SIMILARITY.
 FT DISULFID 33 48 BY SIMILARITY.
 FT DISULFID 38 46 BY SIMILARITY.
 FT DISULFID 46 46 BY SIMILARITY.
 SQ SEQUENCE 67 AA; 7242 MW; ED7C4BCB8A9F57B1 CRC64;

Query Match 19.5%; Score 51.5; DB 1; Length 67;
 Best Local Similarity 25.0%; Pred. No. 7.8;
 Matches 12; Conservative 8; Mismatches 11; Indels 17; Gaps 3;

QY 3 GPCEERKHLFVDPQCKSCSKNTDSRCKARQLEINERTC 45
 DB 3 GPCCDR-----CRCT-KSEPPQCCQDVRLNSCHSACEACVC 38

RESULT 14
 MT3_BOVIN STANDARD; PRT; 68 AA.
 ID MT3_BOVIN
 AC P37359;
 DT 01-OCT-1994 (Rel. 30, Created)
 DT 01-OCT-1994 (Rel. 30, Last sequence update)

```
DT 01-NOV-1997 (Rel. 35, Last annotation update)
DE METALLOTHIONEIN-III (MT-III) (GROWTH INHIBITORY FACTOR) (GIF).
GN MT3.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE.
RC TISSUE=Brain;
RX MEDLINE=94259179; PubMed=8200454;
RA Pountney D.L., Fundel S.M., Faller P., Birchler N.E., Hunziker P.,
RA Vasak M.;
RT "Isolation, primary structures and metal binding properties of
RT neuronal growth inhibitory factor (GIF) from bovine and equine
RT brain."
RL FEBS Lett. 345:193-197(1994).
CC -1- FUNCTION: BINDS HEAVY METALS. CONTAINS FIVE ZINC AND ONE COPPER
CC ATOMS PER POLYPEPTIDE CHAIN AND ONLY A NEGLIGIBLE AMOUNT OF
CC CADMIUM.
CC -1- TISSUE SPECIFICITY: BRAIN.
CC -1- SIMILARITY: BELONGS TO FAMILY 1 IN METALLOTHIONEIN SUPERFAMILY.
CC PIR, S44391; S44391.
DR HSSP; P18055; IMRB.
DR InterPro; IPR003019; Metallthion.
DR InterPro; IPR000006; Metallthion_vert.
DR Pfam; PF00131; metalthio_1.
DR PRINTS; PR00860; MTVERTERATE.
DR PROSITE; PS00203; METALLOTHIONEIN_VRT; 1.
KW Metal-binding; Metal-thiolate cluster; Chelation; Zinc; Copper;
KW Acetylation.
FT MOD_RES 1 1 ACETYLATION.
FT DOMAIN 1 30 BETA.
FT METAL 31 68 ALPHA.
FT METAL 8 6 CLUSTER B (BY SIMILARITY).
FT METAL 6 8 CLUSTER B (BY SIMILARITY).
FT METAL 14 14 CLUSTER B (BY SIMILARITY).
FT METAL 16 16 CLUSTER B (BY SIMILARITY).
FT METAL 20 20 CLUSTER B (BY SIMILARITY).
FT METAL 22 22 CLUSTER B (BY SIMILARITY).
FT METAL 25 25 CLUSTER B (BY SIMILARITY).
FT METAL 27 27 CLUSTER B (BY SIMILARITY).
FT METAL 30 30 CLUSTER B (BY SIMILARITY).
FT METAL 34 34 CLUSTER A (BY SIMILARITY).
FT METAL 35 35 CLUSTER A (BY SIMILARITY).
FT METAL 37 37 CLUSTER A (BY SIMILARITY).
FT METAL 38 38 CLUSTER A (BY SIMILARITY).
FT METAL 42 42 CLUSTER A (BY SIMILARITY).
FT METAL 45 45 CLUSTER A (BY SIMILARITY).
FT METAL 49 49 CLUSTER A (BY SIMILARITY).
FT METAL 51 51 CLUSTER A (BY SIMILARITY).
FT METAL 64 64 CLUSTER A (BY SIMILARITY).
FT METAL 66 66 CLUSTER A (BY SIMILARITY).
FT METAL 67 67 CLUSTER A (BY SIMILARITY).
SQ SEQUENCE 68 AA; 6953 MW; FC824B83AA52B4C0 CRC64;
```

```
Query Match 19.3%; Score 51; DB 1; Length 68;
Best Local Similarity 29.6%; Pred. No. 9;
Matches 16; Conservative 4; Mismatches 16; Indels 18; Gaps 4;
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OY 1 PC---GPCSRKRLHLPQDPQCK-----SKNTDSRCARQLELNEPNCRC 45
DB 7 PCPTGGSCCT-----CSDP--CKBGCCTCASCCKSCCSCCPAECCKACADVC 51
```

```
RESULT 15
MT3 HORSE STANDARD; PRT; 68 AA.
AC P37360;
DT 01-OCT-1994 (Rel. 30, Created)
DT 01-OCT-1994 (Rel. 30, Last sequence update)
```

```
DT 01-NOV-1997 (Rel. 35, Last annotation update)
DE METALLOTHIONEIN-III (MT-III) (GROWTH INHIBITORY FACTOR) (GIF).
GN MT3.
OS Equus caballus (Horse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Perissodactyla; Equidae; Equus.
OX NCBI_TaxID=9796;
RN [1]
RP SEQUENCE.
RC TISSUE=Brain;
RX MEDLINE=94259179; PubMed=8200454;
RA Pountney D.L., Fundel S.M., Faller P., Birchler N.E., Hunziker P.,
RA Vasak M.;
RT "Isolation, primary structures and metal binding properties of
RT neuronal growth inhibitory factor (GIF) from bovine and equine
RT brain."
RL FEBS Lett. 345:193-197(1994).
CC -1- FUNCTION: BINDS HEAVY METALS. CONTAINS THREE ZINC AND THREE COPPER
CC ATOMS PER POLYPEPTIDE CHAIN AND ONLY A NEGLIGIBLE AMOUNT OF
CC CADMIUM.
CC -1- TISSUE SPECIFICITY: BRAIN.
CC -1- SIMILARITY: BELONGS TO FAMILY 1 IN METALLOTHIONEIN SUPERFAMILY.
CC PIR, S44392; S44392.
DR HSSP; P18055; IMRB.
DR InterPro; IPR003019; Metallthion.
DR InterPro; IPR000006; Metallthion_vert.
DR Pfam; PF00131; metalthio_1.
DR PRINTS; PR00860; MTVERTERATE.
DR PROSITE; PS00203; METALLOTHIONEIN_VRT; 1.
KW Metal-binding; Metal-thiolate cluster; Chelation; Zinc; Copper;
KW Acetylation.
FT MOD_RES 1 1 ACETYLATION.
FT DOMAIN 1 30 BETA.
FT METAL 31 68 ALPHA.
FT METAL 8 6 CLUSTER B (BY SIMILARITY).
FT METAL 6 8 CLUSTER B (BY SIMILARITY).
FT METAL 14 14 CLUSTER B (BY SIMILARITY).
FT METAL 16 16 CLUSTER B (BY SIMILARITY).
FT METAL 20 20 CLUSTER B (BY SIMILARITY).
FT METAL 22 22 CLUSTER B (BY SIMILARITY).
FT METAL 25 25 CLUSTER B (BY SIMILARITY).
FT METAL 27 27 CLUSTER B (BY SIMILARITY).
FT METAL 30 30 CLUSTER B (BY SIMILARITY).
FT METAL 34 34 CLUSTER A (BY SIMILARITY).
FT METAL 35 35 CLUSTER A (BY SIMILARITY).
FT METAL 37 37 CLUSTER A (BY SIMILARITY).
FT METAL 38 38 CLUSTER A (BY SIMILARITY).
FT METAL 42 42 CLUSTER A (BY SIMILARITY).
FT METAL 45 45 CLUSTER A (BY SIMILARITY).
FT METAL 49 49 CLUSTER A (BY SIMILARITY).
FT METAL 51 51 CLUSTER A (BY SIMILARITY).
FT METAL 64 64 CLUSTER A (BY SIMILARITY).
FT METAL 66 66 CLUSTER A (BY SIMILARITY).
FT METAL 67 67 CLUSTER A (BY SIMILARITY).
SQ SEQUENCE 68 AA; 6927 MW; 5998E0F17FC52CE6 CRC64;
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Query Match 19.3%; Score 51; DB 1; Length 68;
Best Local Similarity 24.0%; Pred. No. 9;
Matches 12; Conservative 4; Mismatches 14; Indels 20; Gaps 1;
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OY 16 DPQCKC-----SKNTDSRCARQLELNEPNCRC 45
DB 2 DPETCPPTGGSCCTCGCKCGCKTSCCKSCCSCCPAECCKACADVC 51
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Search completed: January 31, 2002, 11:22:32
Job time: 113 sec
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GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: January 31, 2002, 11:19:34 ; Search time 13.28 Seconds

(without alignments)
258.122 Million cell updates/sec

Title: US-09-579-420-1

Perfect score: 264
Sequence: 1 PCGPCSRRKRLHFLVQDPQTC.....NTDSRCKARQLELNERTC 45

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 219241 seqs, 76174552 residues

Total number of hits satisfying chosen parameters: 30440

Minimum DB seq length: 0

Maximum DB seq length: 100

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

1: PIR_68:*
2: PIR1:*
3: PIR3:*
4: PIR4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	58	22.0	83	2	D84697
2	54	20.5	75	2	B45206
3	53.5	20.3	63	2	A34905
4	53.5	20.3	74	2	T24715
5	53	20.1	62	2	I51538
6	53	20.1	63	2	C34620
7	53	20.1	63	2	S33381
8	53	20.1	63	2	A34620
9	53	20.1	63	2	A34938
10	53	20.1	66	2	S58086
11	53	20.1	68	2	A46034
12	53	20.1	68	2	I67866
13	52.5	19.9	69	2	A55011
14	52	19.7	63	2	S08191
15	52	19.7	68	2	B46034
16	51.5	19.5	58	1	SMKDIS
17	51.5	19.3	83	2	A05157
18	51	19.3	68	2	S44392
19	51	19.3	68	2	S44391
20	51	19.3	68	2	JC6521
21	51	19.3	75	2	S17156
22	51	19.3	91	2	S71147
23	49.5	18.8	35	1	S59072
24	49	18.6	35	1	NTSRPM
25	49	18.6	96	2	E64505
26	48.5	18.4	87	2	A39439
27	48.5	18.4	98	2	T42349
28	48	18.2	57	2	S59073
29	48	18.2	81	2	T14444

30	48	18.2	88	2	JC5203	outer membrane pro
31	47.5	18.0	35	2	A24677	Balbani ring 2 ch
32	47.5	18.0	62	2	A53640	metallochionein 4
33	47.5	18.0	71	2	S47576	metallochionein 20
34	47.5	18.0	71	2	S39420	metallochionein 20
35	47.5	18.0	82	1	T12BI	protease inhibitor
36	47.5	18.0	84	2	A61594	thrombospondin - b
37	47.5	18.0	92	2	A72242	ferredoxin - therm
38	47	17.8	57	1	SMKDS	metallochionein 2
39	47	17.8	62	2	S15676	metallochionein 2
40	46.5	17.6	95	2	S01717	chorionic gonadotr
41	46	17.4	50	2	S53431	Balbani ring prot
42	46	17.4	52	2	JC1197	echistatin beta -
43	46	17.4	58	2	S43367	metallochionein 11
44	46	17.4	70	2	T13341	metallochionein -
45	46	17.4	72	2	S39416	hypothetical prote
						metallochionein 10

ALIGNMENTS

RESULT 1
D84697
hypothetical protein At2g29530 [imported] - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 02-Feb-2001
C:Accession: D84697
R:Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.
M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon,
euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter
Nature 402, 761-768, 1999
A:Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.
A:Reference number: AB44420, MIMD:20083487
A:Accession: D84697
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-83 <STO>
A:Cross-references: GB:AE002093; NID:93980383; PIDN:AA095186.1; GSPDB:GN00139
C:Genetics:
A:Gene: At2g29530
A:Map position: 2

Query Match 22.0% Score 58; DB 2; Length 83;
Best Local Similarity 39.0% Pred. No. 11;
Matches 16; Conservative 4; Mismatches 17; Indels 4; Gaps 2;

OY 7 ERRKHLFVQDPQTCCKNTDSRCKARQLELNERTC--RC 45
DB 23 EYRVELFNKLAQTCFNKC--VDRRYKEALNMGENSEIDRC 61

RESULT 2
B45206
metallochionein 2 - Caenorhabditis elegans
N:Alternate names: metallochionein I
C:Species: Caenorhabditis elegans
C:Date: 30-Apr-1993 #sequence_revision 18-Nov-1994 #text_change 29-Oct-1999
C:Accession: B45206; S09714; T29721
R:Freeman, J.H.; Slice, D.W.; Dixon, D.; Fire, A.; Rubin, C.S.
J. Biol. Chem. 268, 2554-2564, 1993
A:Title: The novel metallochionein genes of Caenorhabditis elegans. Structural organi
A:Reference number: A45206; MIMD:93155063
A:Accession: B45206
A>Status: preliminary; not compared with conceptual translation
A:Molecule type: DNA
A:Residues: 1-75 <PRE>
A:Note: sequence extracted from NCBI backbone (NCBI:124147)
R:Imagawa, M.; Onozawa, T.; Okumura, K.; Osada, S.; Nishihara, T.; Kondo, M.
Biochem. J. 268, 237-240, 1990
A:Title: Characterization of metallochionein cDNAs induced by cadmium in the nematode
A:Reference number: S09714; MIMD:90262552
A:Accession: S09714

A:Molecule type: mRNA
 A:Residues: 1-75 <IMA>
 A:Cross-references: EMBL:X53244; NID:g6779; PIDN:CAA37334.1; PID:g6780
 R:Greco, T.; Bradshaw, H.
 submitted to the EMBL Data Library, July 1996
 A:Description: The sequence of C. elegans cosmid K11G9.
 A:Reference number: Z20672
 A:Accession: T29721
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-75 <GRE>
 A:Cross-references: EMBL:U64853; PIDN:AAB04979.1; GSPDB:GN00023; CESP:K11G9.6
 A:Experimental source: strain Bristol N2; clone K11G9
 C:Genetics:
 A:Gene: CESP:K11G9.6
 A:Map position: 5
 A:Introns: 6/1
 C:Superfamily: metallochionein

Query Match 20.5%; Score 54; DB 2; Length 75;
 Best Local Similarity 34.6%; Pred. No. 28;
 Matches 9; Conservative 2; Mismatches 7; Indels 8; Gaps 1;

OY 20 CKCCKNTDSRCKAROLELNERCRC 45
 ||| ||| : : : : :
 Db 3 CKDCCKNKCKCGDK-----CEC 20

RESULT 3
 A34905
 metallochionein 1 - Caenorhabditis elegans
 N:Alternate names: metallochionein Ce; metallochionein II
 C:Species: Caenorhabditis elegans
 C>Date: 20-Jul-1990 #sequence_revision 20-Jul-1990 #text_change 20-Aug-1999
 C:Accession: A45206; A34905; S09715
 R:Freedman, J.H.; Slice, L.W.; Dixon, D.; Fire, A.; Rubin, C.S.
 J. Biol. Chem. 268, 2554-2564, 1993
 A:Title: The novel metallochionein genes of Caenorhabditis elegans. Structural organization
 A:Reference number: A45206; MUID:93155063
 A:Accession: A45206
 A:Status: preliminary; not compared with conceptual translation
 A:Molecule type: DNA
 A:Residues: 1-63 <FRE>
 A:Note: Sequence extracted from NCBI backbone (NCBIP.124145)
 R:Slice, L.W.; Freedman, J.H.; Rubin, C.S.
 J. Biol. Chem. 265, 256-263, 1990
 A:Title: Purification, characterization, and cDNA cloning of a novel metallochionein-like
 A:Reference number: A34905; MUID:90094407
 A:Accession: A34905
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-63 <SLI>
 A:Cross-references: GB:M32386; NID:9156380; PIDN:AAA28117.1; PID:9156381; GB:J05169
 R:Imagawa, M.; Onozawa, T.; Okumura, K.; Osada, S.; Nishihara, T.; Kondo, M.
 Biochem. J. 268, 237-240, 1990
 A:Title: Characterization of metallochionein cDNAs induced by cadmium in the nematode Ca
 A:Reference number: S09714; MUID:90262552
 A:Accession: S09715
 A:Molecule type: mRNA
 A:Residues: 1-63 <IMA>
 A:Cross-references: EMBL:X53245; NID:g6781; PIDN:CAA37335.1; PID:g6782
 C:Superfamily: metallochionein

Query Match 20.3%; Score 53.5; DB 2; Length 63;
 Best Local Similarity 34.6%; Pred. No. 28;
 Matches 9; Conservative 2; Mismatches 10; Indels 5; Gaps 1;

OY 20 CKCCKNTDSRCKAROLELNERCRC 45
 ||| ||| : : : : :
 Db 3 CKDCCKNKCKCGDK-----GTKDCDC 23

RESULT 4
 T24715
 hypothetical protein T08G5.10 - Caenorhabditis elegans
 C:Species: Caenorhabditis elegans
 C>Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 21-Jul-2000
 C:Accession: T24715
 R:Smyle, R.
 submitted to the EMBL Data Library, November 1996
 A:Reference number: Z19927
 A:Accession: T24715
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-74 <WIL>
 A:Cross-references: EMBL:281589; PIDN:CAB04723.1; GSPDB:GN00023; CESP:T08G5.10
 A:Experimental source: clone T08G5
 C:Genetics:
 A:Gene: CESP:T08G5.10
 A:Map position: 5
 A:Introns: 17/1
 C:Superfamily: metallochionein

Query Match 20.3%; Score 53.5; DB 2; Length 74;
 Best Local Similarity 34.6%; Pred. No. 31;
 Matches 9; Conservative 2; Mismatches 10; Indels 5; Gaps 1;

OY 20 CKCCKNTDSRCKAROLELNERCRC 45
 ||| ||| : : : : :
 Db 14 CKDCCKNKCKCGDK-----GTKDCDC 34

RESULT 5
 I51538
 metallochionein - African clawed frog
 C:Species: Xenopus laevis (African clawed frog)
 C>Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 20-Aug-1999
 C:Accession: I51538
 R:Saint-Jacques, E.; Seguin, C.
 DNA Cell Biol. 12, 329-340, 1993
 A:Title: Cloning and nucleotide sequence of a complementary DNA encoding Xenopus laevis
 A:Reference number: I51538; MUID:93263990
 A:Accession: I51538
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 1-62 <SAI>
 A:Cross-references: GB:M96729; NID:g214585; PIDN:AAB59949.1; PID:g214586
 C:Superfamily: metallochionein

Query Match 20.1%; Score 53; DB 2; Length 62;
 Best Local Similarity 33.3%; Pred. No. 31;
 Matches 12; Conservative 2; Mismatches 16; Indels 6; Gaps 1;

OY 16 DPQTC-----CCKNTDSRCKAROLELNERCRC 45
 ||| || : : : : :
 Db 2 DPQCKCETGASCSCGTTCSCKCKSCSC 37

RESULT 6
 C34620
 metallochionein - muscovy duck
 C:Species: Cairina moscovata (muscovy duck)
 C>Date: 22-Jun-1990 #sequence_revision 22-Jun-1990 #text_change 20-Aug-1999
 C:Accession: C34620; JC5094
 R:Liu, L.Y.; Huang, P.C.
 Biochem. Biophys. Res. Commun. 168, 182-187, 1990
 A:Title: Complete homology in metallochionein from two genera of ducks and their hybr
 A:Reference number: A34620; MUID:90226357
 A:Accession: C34620
 A:Status: preliminary
 A:Molecule type: protein
 A:Residues: 1-63 <LIN>

R:Lee, Y.J.; Chen, Y.P.; Wang, S.H.; Chow, W.Y.; Lin, L.Y.
Gene 176, 85-92, 1996

A:Title: Structure and expression of metallothionein gene in ducks.

A:Reference number: JC5094; MUID:97075914

A:Accession: JC5094

A:Molecule type: mRNA

A:Residues: 1-63 <LEE>

A:Cross-references: GB:034230; NID:g1000297; PIDN:AAC0047.1; PID:g1000298

C:Comment: This protein has a high metal binding capacity and sulfur content.

C:GeneCis:

A:Gene: mt

A:Introns: 11/1; 33/1

C:Superfamily: metallothionein

Query Match	20.1%;	Score 53;	DB 2;	Length 63;
Best Local Similarity	30.0%;	Pred. No. 31;		
Matches 12; Conservative	4;	Mismatches 10;	Indels 14;	Gaps 2

```

QY 16 DPQCKC-----SKNTDSCARQLELNERCRC 45
    ||| |      ||| : ||:      | |
db 2 DPQDCTCAAGDSCAGSCCKCNCRS----CRKSCCSC 37

```

RESULT 7
S33381
metallothionein - turkey
C:Species: Meleagris gallopavo (common turkey)
C:Date: 13-Jan-1995 #sequence_rev1510n 13-Jan-1995 #text_change 20-Aug-1999
C:Accession: S33381; S33380; S18180
R:Shartzer, K.L.; Kage, K.; Sobleski, R.J.; Andrews, G.K.
J. Mol. Evol. 36, 255-262, 1993
A:Title: Evolution of avian metallothionein: DNA sequence analyses of the turkey metalld
A:Reference number: S33378; NUID:93247066
A:Accession: S33381
A:Molecule type: DNA
A:Residues: 1-63 <SHA>
A:Cross_references: EMBL:X62513
A:Accession: S33380
A:Molecule type: mRNA
A:Residues: 15-57 <SH2>
A:Cross_references: EMBL:X62514; NID:g64090; PIDN:CAAA4372.1; PID:g64091
C:Genetics:
A:Introns: 11/1, 33/1
C:Superfamily: metallothionein

Query Match	20.1%;	Score 53;	DB 2;	Length 63;
Best Local Similarity	30.0%;	Pred. NO. 31;		
Matches 12; Conservative	4;	Mismatches 10;	Indels 14;	Gaps 2

```

QY 16 DPQTC-----SKNTDSCKARQELNERC 45
    ||| |      ||| : ||: | |
Db 2 DPQDCTCAAGDSCSCAGSCCKNCRCRS---CRKSCCSC 37

```

RESULT 8
A34620
metallothionein - duck
C:Species: *Anas platyrhynchos* (domestic duck)
C:Date: 22-Jun-1990 #sequence_revision 22-Jun-1990 #text_change 20-Aug-1999
C:Accession: A34620; B34620; S13154; JC5095
R:Llin, L.Y.; Huang, P.C.
Biochem. Biophys. Res. Commun. 168, 182-187, 1990
A:Title: Complete homology in metallothionein from two genera of ducks and their hybrids
A:Reference number: A34620; M0ID:90226357
A:Accession: A34620
A:Status: preliminary
A:Molecule type: protein
A:Residues: 1-63 <LIN>
A:Experimental source: *Anas platyrhynchos* (domestic duck)
A:Accession: B34620
A:Status: preliminary

A:Molecule type: protein
A:Residues: 1-63 <LI2>
A:Experimental source: *Anas platyrhynchos* x *Carina moschata* (domestic duck x muscovy duck)
R:Lin, L.Y.; Liu, L.F.; Tam, M.F.; Huang, P.C.; Vestling, M.; Fenselau, C.
B:Biochem. Biophys. Acta 1041, 31-35, 1990
A:Title: Primary sequence of duck metallochionein.
A:Reference number: S13154; MUID:91027866
A:Accession: S13154
A>Status: preliminary
A:Molecule type: Protein
A:Residues: 1-63 <LI3>
R:Lee, Y.J.; Chen, Y.P.; Wang, S.H.; Chow, W.Y.; Lin, L.Y.
Gene 176, 85-92, 1996
A:Title: Structure and expression of metallochionein gene in ducks.
A:Reference number: JCS094; MUID:97075914
A:Accession: JCS094

A:Gene: mt
A:Introns: 11/1, 33/1
C:Superfamily: metallothionein

```

QY 16 DPQCKC-----SKNTDSRCKARQLELNEKTCRC 45
    ||| |      ||| : ||: | |
Db 2 DPQDTCAGAGDSCSCAGCKCKNCRCRS----CRKSCCSC 37

```

RESULT 9

A34958
metallothionein - chicken
C:Species: Gallus gallus (chicken)
C:Date: 13-Jul-1990 #sequence_revision 13-Jul-1990 #text_change 20-Aug-1999
C:Accession: A34958; S01750; J00030; A28113
R:Fernando, L.P.; Wei, D.; Andrews, G.K.
J. Nutr. 119, 309-316, 1989
A>Title: Structure and expression of chicken metallothionein.
A:Reference number: A34958; MUID:89141100
A:Accession: A34958
A>Status: preliminary; not compared with conceptual translation
A:Molecule type: mRNA
A:Residues: 1-63 <FER>
R:Wei, D.; Andrews, G.K.
Nucleic Acids Res. 16, 537-553, 1988
A>Title: Molecular cloning of chicken metallothionein. Deduction of the complete amino
A:Reference number: S01750; MUID:88124253
A:Accession: S01750
A:Molecule type: mRNA
A:Residues: 1-63 <WEI>
A:Cross-references: EMBL:X06749; NID:963617; PIDN:CAA29924.1; PID:963618
A>Note: part of this sequence, including the amino end of the mature protein, was con
R:Fernando, L.P.; Andrews, G.K.
Gene 81, 177-183, 1989
A>Title: Cloning and expression of an avian metallothionein-encoding gene.
A:Reference number: J00030; MUID:90034180
A:Accession: J00030
A:Molecule type: DNA
A:Residues: 1-63 <FE2>
R:McCormick, C.C.; Fullmer, C.S.; Garvey, J.S.
Proc. Natl. Acad. Sci. U.S.A. 85, 309-313, 1988
A>Title: Amino acid sequence and comparative antigenicity of chicken metallothionein.
A:Reference number: A28113; MUID:88124831
A:Accession: A28113
A:Molecule type: protein
A:Residues: 1-63 <MCC>

A:Experimental source: liver
C:Comment: Metallothioneins are a class of cysteine-rich, heavy-metal-binding proteins
C:Genetics:
A:Gene: CMT
A:Introns: 11/1; 33/1
C:Superfamily: metallothionein
C:1-63/Product: metallothionein #status experimental <MAT>

Query Match	20.1;	Score 53;	DB 2;	Length 63;
Best Local Similarity	30.08;	Pred. No. 31;		
Matches 12; Conservative	4;	Mismatches 14;	Gaps 2;	

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Qy      16 DPQTKC-----SCNTDSRCARQLELNEBTCRC 45
          ||| |      ||| : ||::      : | |
Db      2  DPQDTCAAGDSCCAGSCCKNCRCS---CRKSCCSC 37

```

```

RESULT 10
S58086
metalothionein 3 - rat
N:Alternate names: neurotrophic growth inhibitory factor
C:Species: Rattus norvegicus (Norway rat)
C:Date: 13-Jan-1996 #sequence_rev150n 19-Apr-1996 #text_change 20-Aug-1999
C:Accession: S58086: 152636
R:Amoureux, M.C.; Rethaus, E.; Wurch, T.; Colpaert, F.C.; Pauwels, P.J.
Submitted to the EMBL Data Library, July 1995
:Reference number: S58084

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A:Accession: S58086
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-66 <AM>
A:Cross-references: EMBL:X89603; NID:G908880; PIDN:CA61762.1; PID:G908881
R:Kobayashi, H.; Uchida, Y.; Ihara, Y.; Nakajima, K.; Kobaka, S.; Miyatake, T.; Tsuji, R.
Brain Res. Mol. Brain Res. 19, 188-194, 1993
A>Title: Molecular cloning of rat growth inhibitory factor cDNA and the expression in th
A:Reference number: I52636; MUID:94018480
A:Accession: I52636

A:Status: preliminary; translated from GR/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-66 <KB>
A:Cross-references: GR:S65838; NID:g425381; PIDD:AMB28366.1; PID:g425382
C:Superfamily: metallothionein
C:Keywords: acetylated amino end; chelation; metal binding; metal-thiolate cluster
F:1/Modified site: acetylated amino end (Met) #status predicted
F:6,16,17,38,20,22,25,27,30/Binding site: transition metal ions (Cys) #status predicted
F:3,4,35,37,38,42,45,49,51,62,64,65/Binding site: transition metal ions (Cys) #status predicted

Query Match	20.1%	Score 53	DB 2	length 66
Best Local Similarity	35.3%	Pred. NO. 32		
Matches 12; Conservative	5;	Mismatches 12;	Indels 3;	Gaps 3;

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Qy      16 DPQTCCK----SCKNTDSRCKARQLENERTCRC 455
          ||: || |      || : : ||      : ||:
Db      2  DPETCPCPPTGGSCCTSD-KCKC-----KGCKC 27

```

```

RESULT 11
A46034
metallothionein 3, brain-specific - mouse
N:Alternate names: neurotrophic growth inhibitory factor
C:Species: Mus musculus (house mouse)
C:Date: 21-Sep-1993 #sequence_revision 18-Nov-1994 #text_change 20-Aug-1999
C:Accession: A46034
R:Palmiter, R.D.; Findley, S.D.; Whitmore, T. E.; Durnam, D.M.
Proc. Natl. Acad. Sci. U.S.A. 89, 6333-6337, 1992
A:Title: Mn-Ti1, a brain-specific member of the metallothionein gene family
:Reference number: A46034; MUID:92335292

```

A:Cross-references: GB:M93310: NID:g199133: PIDN:AAA39529_1: PID:g199134
 A:Note: sequence extracted from NCBI backbone (NCBIN:108715, NCBIN:111115, NCBIP:1087
 C:Superfamily: metallohydrolase

Query Match	20.1%;	Score 53;	DB 2;	Length 68;
Best Local Similarity	35.3%;	Pred. No. 33;		
Matches 12; Conservative	5;	Mismatches	12;	Gaps 3

```

QY      16 DPQCTKC-----SCKNTDSRCKARQLELNEPTCRC 45
          ||::|| |      ||::||: ||: ||
Db       2 DPETPCPTGGSGCTCSD-KCKC-----KGCKC 27

```

RESULT 12
167866
growth inhibitory factor - mouse
C:Species: Mus sp. (mouse)
C:Date: 29-May-1998 #sequence.revision 29-May-1998 #text.change 20-Aug-1999
C:Accession: 167866
R:Naruse, S.; Igarashi, S.; Furuya, T.; Kobayashi, H.; Miyatake, T.; Tsuji, S.
Gene 144, 283-287, 1994
A:Title: Structures of the human and mouse growth inhibitory factor-encoding genes
A:Reference number: I53803; MUID:94314230
A:Accession: 167866
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-68 <RES>
A:Cross-references: GB:S72046; NID:g565191; PIDN:AAB31397.1; PID:g565192
C:Genetics:
A:Gene: GIF
A:Introns: 11/1; 33/1
A:Superfamily: metallohonein

Query Match	20.1%	Score 53;	DB 2;	Length 68;
Best Local Similarity	35.38%	Pred. No. 33;		
Matches 12; Conservative		5; Mismatches	12; Indels	Gaps 3;

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QY      16 DPQYCKC-----SCKNTDSRCKARQLEINERTCR 45
          ||: || |      || : : ||      : ||: |
Db      2 DPETCPCPYTGSGCTSD-KCKC-----KGCKC 27

```

RESULT 13
A55011
metallothionein-like protein YOR031w - Yeast (Saccharomyces cerevisiae)
N:Alternate names: protein 02675
C:Species: Saccharomyces cerevisiae
C:Date: 11-Nov-1994 #sequence_revstion 11-Nov-1994 #ext-change 21-Jul-2000
C:Accession: A55011; S66897
R:Cutotta, V.C.; Howard, W.R.; Liu, X.F.
J. Biol. Chem. 269, 25295-25302, 1994
A:Title: CRS5 encodes a metallothionein-like protein in Saccharomyces cerevisiae
A:Reference number: A55011; M0ID:J95014318
A:Accession: A55011
A:Molecule type: DNA
A:Residues: 1-69 <CU>
A:Cross-references: GB:I29056; MID:g49891; PIDN:AAA66061.1; PID:g499892
R:de Haan, M.; Grivell, L.A.; Maarsee, A.C.
submitted to the Protein Sequence Database, July 1996
A:Reference number: S66877
A:Accession: S66897
A:Molecule type: DNA
A:Residues: 1-8 <DEH>
A:Note: in strain S288C YOR031w is a pseudogene with an inframe stopcodon
A:Experimental source: EMBL:I74939; MIPS:YOR031w
A:Note: in strain S288C YOR031w is a pseudogene with an inframe stopcodon
C:Genetics:
A:Gene: CRS5
A:Map position: 15R
A:Note: YOR031w
A:Function:

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GenCore version 4.5
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OM protein - protein search, using sw model

Run on: January 31, 2002, 11:19:09 ; Search time 12.47 Seconds
(without alignments)
81.207 Million cell updates/sec

Title: US-09-579-420-1

Perfect score: 264
Sequence: 1 PCGPCSERRRHLEFYQDPQTC.....NTDSRCAROLELNERTCRC 45

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 212252 seqs, 22503292 residues

Total number of hits satisfying chosen parameters: 162600

Minimum DB seq length: 0

Maximum DB seq length: 100

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Issued_Patents_AA:*
1: /cgn2_6/ptodata/2/1aa/5A.COMB.pep:*
2: /cgn2_6/ptodata/2/1aa/5B.COMB.pep:*
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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed.
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	115	43.6	55	1	US-08-469-427A-3
2	115	43.6	55	2	US-08-609-443B-3
3	115	43.6	55	2	US-08-569-063C-3
4	105	39.8	18	3	US-08-807-992B-28
5	100	37.9	17	3	US-08-807-992B-29
6	76	28.8	19	3	US-08-807-992B-7
7	76	28.8	19	3	US-08-807-992B-13
8	76	28.8	19	3	US-08-807-992B-16
9	76	28.8	19	3	US-08-807-992B-30
10	52	19.7	68	1	US-07-696-051B-1
11	52	19.7	68	1	US-07-924-063A-1
12	52	19.7	68	1	US-08-138-340B-2
13	52	19.7	97	2	US-08-726-306A-128
14	50	18.9	49	4	US-09-020-880-14
15	50	18.9	49	4	US-09-020-880-16
16	48	18.2	94	4	US-09-020-880-18
17	48	18.2	94	4	US-08-226-264-22
18	47.5	18.0	26	1	US-08-138-340B-3
19	47	17.8	53	4	US-08-284-923-2
20	47	17.8	53	4	US-08-619-032B-2
21	47	17.8	100	3	US-08-965-903B-11
22	46.5	17.6	86	2	US-08-465-380-45
23	46.5	17.6	86	2	US-08-486-397-45
24	46.5	17.6	86	2	US-08-486-399-45
25	46.5	17.6	86	2	US-08-461-965-45
26	46.5	17.6	86	2	US-08-634-641-45
27	46.5	17.6	86	3	US-09-249-471-45

28	46.5	17.6	86	3	US-09-249-472-45	Sequence 45, Appl
29	46.5	17.6	86	3	US-09-249-451-45	Sequence 45, Appl
30	46.5	17.6	86	3	US-08-809-455-45	Sequence 45, Appl
31	46.5	17.6	86	3	US-09-249-461-45	Sequence 45, Appl
32	46.5	17.6	86	3	US-09-249-448-45	Sequence 45, Appl
33	46	17.4	53	6	5332669-2	Patent No. 5332669
34	46	17.4	58	3	US-08-904-446A-14	Sequence 14, Appl
35	46	17.4	76	4	US-08-866-545-4	Sequence 4, Appl
36	45.5	17.2	48	2	US-08-465-794-3	Sequence 3, Appl
37	45.5	17.2	48	3	US-09-049-813-3	Sequence 3, Appl
38	45.5	17.2	58	4	US-08-866-545-10	Sequence 10, Appl
39	45.5	17.2	58	3	US-08-904-446A-15	Sequence 15, Appl
40	45.5	17.2	61	2	US-08-453-051-2	Sequence 2, Appl
41	45.5	17.2	73	1	US-08-379-538-7	Sequence 7, Appl
42	45.5	17.2	80	4	US-08-663-191A-3	Sequence 3, Appl
43	45.5	17.2	86	4	US-09-051-624A-2	Sequence 2, Appl
44	45.5	17.2	86	2	US-08-465-380-46	Sequence 46, Appl
45	45.5	17.2	86	2	US-08-486-397-46	Sequence 46, Appl

ALIGNMENTS

RESULT 1
US-08-469-427A-3
; Sequence 3, Application US/08469427A
; Patent No. 5607918
; GENERAL INFORMATION:
; APPLICANT: Eriksson, Ulf
; APPLICANT: Olofsson, Birgitta
; APPLICANT: Allitalo, Kari
; APPLICANT: Pajusola, Katri
; TITLE OF INVENTION: VASCULAR ENDOTHELIAL GROWTH FACTOR-B AND
; TITLE OF INVENTION: DNA CODING THEREFOR
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Evenson, McKeown, Edwards & Lenahan
; STREET: 1200 G Street, N.W., Suite 700
; CITY: Washington
; STATE: DC
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/469,427A
; FILING DATE: 06-JUN-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/397,651
; FILING DATE: 01-MAR-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Evans, Joseph D
; REGISTRATION NUMBER: 26,269
; REFERENCE/DOCKET NUMBER: 419799cp2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 628-8800
; TELEFAX: (202) 628-8844
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 55 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHEICAL: NO
; ORIGINAL SOURCE:
; TISSUE TYPE: mouse embryo
; US-08-469-427A-3

Query Match 43.6%; Score 115; DB 1; Length 55;
Best Local Similarity 46.7%; Pred. No. 6.2e-07;
Matches 21; Conservative 7; Mismatches 13; Indels 4; Gaps 2;

OY 2 CGPCSERKHLFVQDPOTCKSCSKNTD-SRCKAROLELNERTCRC 45
DB 9 CPPTQORROR---PDPRTCRRCRRRRFLHCQGRGLELNDPTCRC 50

RESULT 2
US-08-609-443B-3
Sequence 3, Application US/08609443B
Patent No. 5840693
GENERAL INFORMATION:
APPLICANT: ERIKSSON, Ulf
APPLICANT: OLOFSSON, Birgitta
APPLICANT: ALTAALO, Kari
APPLICANT: PAJUSOLA, Katri
TITLE OF INVENTION: VASCULAR ENDOTHELIAL GROWTH FACTOR-B AND
TITLE OF INVENTION: DNA CODING THEREFOR
NUMBER OF SEQUENCES: 57
CORRESPONDENCE ADDRESS:
ADDRESSEE: Evenson, McKeown, Edwards & Lenahan, P.L.L.C.
STREET: 1200 G Street, N.W., Suite 700
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/609,443B
FILING DATE: 01-MAR-1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/397,651
FILING DATE: 01-MAR-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/469,427
FILING DATE: 06-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/569,063
FILING DATE: 06-DEC-1995
ATTORNEY/AGENT INFORMATION:
NAME: EVANS, Joseph D
REGISTRATION NUMBER: 26,269
REFERENCE/DOCKET NUMBER: 1064/41979CP4
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 628-8800
TELEFAX: (202) 628-8844
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 55 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
ORIGINAL SOURCE:
TISSUE TYPE: mouse embryo
US-08-609-443B-3

Query Match 43.6%; Score 115; DB 2; Length 55;
Best Local Similarity 46.7%; Pred. No. 6.2e-07;
Matches 21; Conservative 7; Mismatches 13; Indels 4; Gaps 2;

OY 2 CGPCSERKHLFVQDPOTCKSCSKNTD-SRCKAROLELNERTCRC 45
DB 9 CPPTQORROR---PDPRTCRRCRRRRFLHCQGRGLELNDPTCRC 50

RESULT 3
US-08-569-063C-3
Sequence 3, Application US/08569063C
Patent No. 5928939
GENERAL INFORMATION:
APPLICANT: ERIKSSON, Ulf
APPLICANT: OLOFSSON, Birgitta
APPLICANT: ALTAALO, Kari
APPLICANT: PAJUSOLA, Katri
TITLE OF INVENTION: VASCULAR ENDOTHELIAL GROWTH FACTOR-B AND
TITLE OF INVENTION: DNA CODING THEREFOR
NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESS:
ADDRESSEE: Evenson, McKeown, Edwards & Lenahan, P.L.L.C.
STREET: 1200 G Street, N.W., Suite 700
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/569,063C
FILING DATE: 06-DEC-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/469,427
FILING DATE: 06-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/397,651
FILING DATE: 01-MAR-1995
ATTORNEY/AGENT INFORMATION:
NAME: EVANS, Joseph D
REGISTRATION NUMBER: 26,269
REFERENCE/DOCKET NUMBER: 1064/41979CP3
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 628-8800
TELEFAX: (202) 628-8844
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 55 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
ORIGINAL SOURCE:
TISSUE TYPE: mouse embryo
US-08-569-063C-3

Query Match 43.6%; Score 115; DB 2; Length 55;
Best Local Similarity 46.7%; Pred. No. 6.2e-07;
Matches 21; Conservative 7; Mismatches 13; Indels 4; Gaps 2;

OY 2 CGPCSERKHLFVQDPOTCKSCSKNTD-SRCKAROLELNERTCRC 45
DB 9 CPPTQORROR---PDPRTCRRCRRRRFLHCQGRGLELNDPTCRC 50

RESULT 4
US-08-807-992B-28
Sequence 28, Application US/08807992B
Patent No. 6022541
GENERAL INFORMATION:
APPLICANT: Senger, Donald R
APPLICANT: Dvorak, Harold F
TITLE OF INVENTION: Immunological preparation for concurrent
specific binding to spatially exposed regions of vascular

```

ATTORNEY/AGENT INFORMATION:
: NAME: David Prashker, Esq.
: REGISTRATION NUMBER: 29,693
: REFERENCE/DOCKET NUMBER: BIS-033
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (978) 525-3194
: INFORMATION FOR SEQ ID NO: 29:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 17 amino acids
: TYPE: amino acid
: STRANDEDNESS: single
: TOPOLOGY: linear
: MOLECULE TYPE: peptide
: FRAGMENT TYPE: internal
:
US-08-807-9928-29

Query Match 37.9%; Score 100; DB 3; Length 17;
Best Local Similarity 100.0%; Pred. No. 1e-05;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 18 QTCKGCKNTDNRCKAR 34
|||||
Db 1 QTCKGCKNTDNRCKAR 17

RESULT 6
US-08-807-9928-7
: Sequence 7, Application US/088079928
: Patent No. 6022541
: GENERAL INFORMATION:
: APPLICANT: Senger, Donald R
: APPLICANT: Dvorak, Harold F
: TITLE OF INVENTION: Immunological preparation for concurrent
: TITLE OF INVENTION: specific binding to spatially exposed regions of vascular
: TITLE OF INVENTION: permeability factor bound in-vivo to a tumor associated bio
: NUMBER OF SEQUENCES: 31
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: David Prashker, Esq.
: STREET: P.O. Box 5387
: CITY: Magnolia
: STATE: Massachusetts

```

```

COMPUTER READABLE FORM:
1 MEDIUM TYPE: Diskette, 3.50 inch, 1.40 Mb storage
2
3 COMPUTER: IBM PS/1
4 OPERATING SYSTEM: MS DOS
5 SOFTWARE: Wordperfect version 5.1
6 CURRENT APPLICATION DATA:
7 APPLICATION NUMBER: US/08/807,992B
8 FILING DATE: March 3, 1997
9 CLASSIFICATION: 424
10 ATTORNEY/AGENT INFORMATION:
11 NAME: David Prasniker, Esq.
12 REGISTRATION NUMBER: 29,693
13 REFERENCE/DOCKET NUMBER: BIS-033
14 TELECOMMUNICATION INFORMATION:
15 TELEPHONE: (978) 525-3794
16 INFORMATION FOR SEO ID NO: 7:
17
18 SEQUENCE CHARACTERISTICS:
19 LENGTH: 19 amino acids
20
21 TYPE: amino acid
22 STRANDEDNESS: single
23 TOPOLOGY: linear
24
25 US-08-807-992B-7

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OY 32 KAROLELNEBTCRC 45
DB 1 KAROLELNEBTCRC 14

RESULT 7

US-08-807-992B-13
Sequence 13, Application US/08807992B
Patent No. 6022541
GENERAL INFORMATION:
APPLICANT: Senger, Donald R
APPLICANT: Dvorak, Harold F
TITLE OF INVENTION: Immunological preparation for concurrent
TITLE OF INVENTION: specific binding to spatially exposed regions of vascular
TITLE OF INVENTION: permeability factor bound in-vivo to a tumor associated blood
NUMBER OF SEQUENCES: 31
CORRESPONDENCE ADDRESSES:
ADDRESSEE: David Prashker, Esq.
STREET: P.O. Box 5387
CITY: Magnolia
STATE: Massachusetts
COUNTRY: USA
ZIP: 01930
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.40 Mb storage
COMPUTER: IBM PS/1
OPERATING SYSTEM: MS DOS
SOFTWARE: Wordperfect version 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/807,992B
FILING DATE: March 3, 1997
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: David Prashker, Esq.
REGISTRATION NUMBER: 29,693
REFERENCE/DOCKET NUMBER: BIS-033
TELECOMMUNICATION INFORMATION:
TELEPHONE: (978) 525-3794
INFORMATION FOR SEO ID NO: 13;
SEQUENCE CHARACTERISTICS:
LENGTH: 19 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-807-992B-13

Query Match 28.8%; Score 76; DB 3; Length 19;
Best Local Similarity 100.0%; Pred. No. 0.0066;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 32 KAROLELNEBTCRC 45
DB 1 KAROLELNEBTCRC 14

RESULT 8
US-08-807-992B-16
Sequence 16, Application US/08807992B
Patent No. 6022541
GENERAL INFORMATION:
APPLICANT: Senger, Donald R
APPLICANT: Dvorak, Harold F
TITLE OF INVENTION: Immunological preparation for concurrent
TITLE OF INVENTION: specific binding to spatially exposed regions of vascular
TITLE OF INVENTION: permeability factor bound in-vivo to a tumor associated blood
NUMBER OF SEQUENCES: 31
CORRESPONDENCE ADDRESSES:
ADDRESSEE: David Prashker, Esq.
STREET: P.O. Box 5387
CITY: Magnolia

STATE: Massachusetts
COUNTRY: USA
ZIP: 01930
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.40 Mb storage
COMPUTER: IBM PS/1
OPERATING SYSTEM: MS DOS
SOFTWARE: Wordperfect version 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/807,992B
FILING DATE: March 3, 1997
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: David Prashker, Esq.
REGISTRATION NUMBER: 29,693
REFERENCE/DOCKET NUMBER: BIS-033
TELECOMMUNICATION INFORMATION:
TELEPHONE: (978) 525-3794
INFORMATION FOR SEO ID NO: 16;
SEQUENCE CHARACTERISTICS:
LENGTH: 19 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-807-992B-16

Query Match 28.8%; Score 76; DB 3; Length 19;
Best Local Similarity 100.0%; Pred. No. 0.0066;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 32 KAROLELNEBTCRC 45
DB 1 KAROLELNEBTCRC 14

RESULT 9
US-08-807-992B-30
Sequence 30, Application US/08807992B
Patent No. 6022541
GENERAL INFORMATION:
APPLICANT: Senger, Donald R
APPLICANT: Dvorak, Harold F
TITLE OF INVENTION: Immunological preparation for concurrent
TITLE OF INVENTION: specific binding to spatially exposed regions of vascular
TITLE OF INVENTION: permeability factor bound in-vivo to a tumor associated bio
NUMBER OF SEQUENCES: 31
CORRESPONDENCE ADDRESSES:
ADDRESSEE: David Prashker, Esq.
STREET: P.O. Box 5387
CITY: Magnolia
STATE: Massachusetts
COUNTRY: USA
ZIP: 01930
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.40 Mb storage
COMPUTER: IBM PS/1
OPERATING SYSTEM: MS DOS
SOFTWARE: Wordperfect version 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/807,992B
FILING DATE: March 3, 1997
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: David Prashker, Esq.
REGISTRATION NUMBER: 29,693
REFERENCE/DOCKET NUMBER: BIS-033
TELECOMMUNICATION INFORMATION:
TELEPHONE: (978) 525-3794
INFORMATION FOR SEO ID NO: 30;
SEQUENCE CHARACTERISTICS:
LENGTH: 19 amino acids

TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
FRAGMENT TYPE: internal
US-08-807-992B-30

Query Match 28.8%; Score 76; DB 3; Length 19;
Best Local Similarity 100.0%; Pred. No. 0.0066;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY - 32 KAROLELNERTCNC 45
DB 1 KAROLELNERTCNC 14

RESULT 10
US-07-696-051B-1
Sequence 1, Application US/07696051B
Patent No. 5214031

GENERAL INFORMATION:

APPLICANT: Tsuji, Shoji
APPLICANT: Miyatake, Tadashi
APPLICANT: Uchida, Yoko
APPLICANT: Ihara, Yasuo
TITLE OF INVENTION: GROWTH-INHIBITORY FACTOR AND CDNA CODING
TITLE OF INVENTION: FOR GROWTH-INHIBITORY FACTOR
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESSEE: Jordan B. Bierman, BIERMAN AND MUSERLIAN
STREET: 757 Third Avenue
CITY: New York
STATE: New York
COUNTRY: USA

ZIP: 10017

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/07/696,051B

FILING DATE: 19910506

CLASSIFICATION: 514

PRIOR APPLICATION DATA:

APPLICATION NUMBER: JP 119620/1990

FILING DATE: 09-MAY-1990

PRIOR APPLICATION DATA:

APPLICATION NUMBER: JP 410164/1990

FILING DATE: 13-DEC-1990

PRIOR APPLICATION DATA:

APPLICATION NUMBER: JP 410165/1990

FILING DATE: 13-DEC-1990

ATTORNEY/AGENT INFORMATION:

NAME: Bierman, Jordan B.

REGISTRATION NUMBER: 18,629

REFERENCE/DOCKET NUMBER: TSU-16

TELECOMMUNICATION INFORMATION:

TELEPHONE: (212)752-7550

TELEFAX: (212)888-6426

TELEX: PATENLIAW (VIA ITT)

INFORMATION FOR SEQ ID NO: 1:

SEQUENCE CHARACTERISTICS:

LENGTH: 68 amino acids

TYPE: AMINO ACID

TOPOLOGY: linear

MOLECULE TYPE: peptide

HYPOTHETICAL: NO

ANTI-SENSE: NO

ORIGINAL SOURCE:

ORGANISM: Homo sapiens

TISSUE TYPE: Cerebral cortex

FEATURE:
NAME/KEY: Peptide
LOCATION: 1..68
OTHER INFORMATION: /note="Growth inhibitory activity
OTHER INFORMATION: on brain cells"
US-07-696-051B-1

Query Match 19.7%; Score 52; DB 1; Length 68;
Best Local Similarity 38.2%; Pred. No. 14;
Matches 13; Conservative 2; Mismatches 7; Indels 12; Gaps 3;

OY 16 DPOTCKC-----SCNNTDSRKAROLELNERTCNC 45
DB 2 DPETCPGSGSGCTCADC-CNC-----EGCKC 27

RESULT 11
US-07-924-063A-1
Sequence 1, Application US/07924063A
Patent No. 5489514

GENERAL INFORMATION:

APPLICANT: TSUJI, SHOJI; MIYATAKE, TADASHI; UCHIDA, YOKO;
APPLICANT: IHARA, YASUO
TITLE OF INVENTION: DNA CODING FOR GROWTH-INHIBITORY FACTOR AND
TITLE OF INVENTION: USE THEREOF
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: BIERMAN & MUSERLIAN
STREET: 600 THIRD AVENUE
CITY: NEW YORK
STATE: NEW YORK
COUNTRY: USA

ZIP: 10016

COMPUTER READABLE FORM:

MEDIUM TYPE: FLOPPY DISK

COMPUTER: IBM PC COMPATIBLE

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: WORDPERFECT 5.1

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/07/924,063A

FILING DATE: 19920828

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: PCT/JP91/01714

FILING DATE: 13-DEC-1991

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 410165/1990

FILING DATE: 13-DEC-1990

ATTORNEY/AGENT INFORMATION:

NAME: CHARLES A. MUSERLIAN

REGISTRATION NUMBER: 19,683

REFERENCE/DOCKET NUMBER: TSU-23

TELECOMMUNICATION INFORMATION:

TELEPHONE: 212-661-8000

TELEFAX: 212-661-8002

INFORMATION FOR SEQ ID NO: 1:

SEQUENCE CHARACTERISTICS:

LENGTH: 68 amino acids

TYPE: AMINO ACID

STRANDEDNESS: Single

TOPOLOGY: linear

MOLECULE TYPE: protein

HYPOTHETICAL: NO

ORGANISM: human

INDIVIDUAL ISOLATE:

DEVELOPMENTAL STAGE:

HAPLOTYPE:

TISSUE TYPE: brain

CELL TYPE:

CELL LINE:


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; EARLIER APPLICATION NUMBER: US 60/037,581
; EARLIER FILING DATE: 1997-02-10
; NUMBER OF SEQ ID NOS: 116
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 14
; LENGTH: 49
; TYPE: PRT
; ORGANISM: No. 6136558 relevant (recombinant)
US-09-020-880-14
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Query Match          18.9%; Score 50; DB 4; Length 49;
Best Local Similarity 31.6%; Pred. No. 17;
Matches 12; Conservative 4; Mismatches 12; Indels 10; Gaps 2;
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Db - 6 CAEKETFCVNGGECFVWVKDPSRYLCKCPNEFTGDRCQ 43
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RESULT 15
US-09-020-880-16
; Sequence 16, Application US/09020880A
; Patent No. 6136558
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; APPLICANT: Ballinger, Marcus D.
; APPLICANT: Jones, Jennifer T.
; APPLICANT: Fairbrother, Wayne J.
; APPLICANT: Sliwkowski, Mark X.
; APPLICANT: Wells, James A.
; TITLE OF INVENTION: HEREGULIN VARIANTS
; FILE REFERENCE: 14918-720CON1
; CURRENT APPLICATION NUMBER: US/09/020,880A
; CURRENT FILING DATE: 1998-02-09
; EARLIER APPLICATION NUMBER: US 60/037,581
; EARLIER FILING DATE: 1997-02-10
; NUMBER OF SEQ ID NOS: 116
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 16
; LENGTH: 49
; TYPE: PRT
; ORGANISM: No. 6136558 relevant (recombinant)
US-09-020-880-16
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Query Match          18.9%; Score 50; DB 4; Length 49;
Best Local Similarity 31.6%; Pred. No. 17;
Matches 12; Conservative 4; Mismatches 12; Indels 10; Gaps 2;
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OY 5 CSERRKH-----LFVODPOTCKCCKN--TDSRCK 32
   1:1:1 1:1:1 1:1:1 1:1:1 1:1:1
Db 6 CAEKETFCVNGGECFVWVKDPSRYLCKCPNEFTGDRCQ 43
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Job time: 138 sec

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